

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2005, 01:55:29 ; Search time 1933 Seconds  
(without alignments)  
10030.407 Million cell updates/sec

Title: US-10-786-065-3\_COPY\_50000\_50409

Perfect score: 410

Sequence: 1 aatcagataatcatcgag.....attatgctgagcttctga 410

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pi.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	410	100.0	5332	6	AR265351 Sequence
2	410	100.0	5332	6	AX571875 Sequence
3	374.4	91.3	112748	9	AC007242 Homo sapi
4	127.4	31.1	2422	9	AK091710 Homo sapi
5	87.4	21.3	2203	6	AR265350 Sequence
6	87.4	21.3	2203	6	AX571873 Sequence
7	75.8	18.5	161010	2	AC132361 Mus muscu
8	75.8	18.5	173131	10	AC116995 Mus muscu
9	71.4	17.4	179341	2	AC128908 Rattus no
10	71.4	17.4	295449	2	AC105819 Rattus no
11	68	16.6	1828	9	AK131512 Homo sapi
12	67	16.3	888	6	AX803407 Sequence
13	66	16.1	481	6	AR175616 Sequence
14	66	16.1	481	6	AR236733 Sequence
15	66	16.1	1077	6	AX056403 Sequence
16	66	16.1	1308	6	AR265352 Sequence
17	66	16.1	1308	6	AX571876 Sequence
18	66	16.1	1308	6	AX772798 Sequence
19	66	16.1	1376	6	AX644241 Sequence

20	66	16.1	1534	6	AX772791	AX772791 Sequence
21	66	16.1	1534	6	AX772795	AX772795 Sequence
22	66	16.1	1534	9	AB053308	AB053308 Homo sapi
23	66	16.1	1584	6	AX772794	AX772794 Sequence
24	66	16.1	1628	6	AX772799	AX772799 Sequence
25	66	16.1	2305	9	BC038807	BC038807 Homo sapi
26	64.4	15.7	3675	9	HSM807539	BM647394 Homo sapi
27	48.2	11.8	7218	6	I66494	I66494 Sequence 14
28	43.2	10.5	204534	2	AC084400	AC084400 Mus muscu
29	43	10.5	82604	9	AL500522	AL500522 Homo sapi
30	43	10.5	166387	2	AC145234	AC145234 Homo sapi
31	42.2	10.3	112510	2	AC120200	AC120200 Dancio ror
32	42.2	10.3	158694	2	AC144471	AC144471 Felis cat
33	41.6	10.1	153539	2	AL591168	AL591168 Homo sapi
34	41.6	10.1	223196	2	AC129035	AC129035 Rattus no
35	41.6	10.1	286395	2	AC125732	AC125732 Rattus no
36	41.6	10.1	292171	2	AC091244	AC091244 Rattus no
37	41.6	10.1	326700	2	AC134362	AC134362 Rattus no
38	41.6	10.1	332668	2	AC130158	AC130158 Rattus no
39	41.6	10.1	333622	2	AC111475	AC111475 Rattus no
40	41.2	10.0	153647	9	AP002979	AP002979 Homo sapi
41	41.2	10.0	167139	9	AC087710	AC087710 Homo sapi
42	41.2	10.0	168736	2	AC019042	AC019042 Homo sapi
43	41.2	10.0	213751	10	AC124524	AC124524 Mus muscu
44	41	10.0	75153	2	AC100376	AC100376 Mus muscu
45	41	10.0	146974	10	AC121919	AC121919 Mus muscu

## ALIGNMENTS

RESULT 1	AR265351	Sequence 3 from patent US 6492154.	5332 bp	DNA	linear	PAT 10-APR-2003
LOCUS	AR265351					
DEFINITION	AR265351					
ACCESSION	AR265351					
VERSION	AR265351.1	GI:29693854				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 5332)					
AUTHORS	Yan, C., Ketchum, K.A., Di Francesco, V. and Beasley, E.M.					
TITLE	Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof					
JOURNAL	Patent: US 6492154-A 3 10-DEC-2002;					
FEATURES	Location/Qualifiers					
source	1..5332					
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Db	50000	AATCATGATTAATCATGAGTAATGTTTCACTGATGAGAACATGACTTTGAGCAAGGCTG	50059		
Qy	61	TATGATGCTGCTGAGAACAGTGTGTAAGTAATGAGCGCCCGGACCATAGGAATGT	120		
Db	50060	TATGATGCTGCTGAGAACAGTGTGTAAGTAATGAGCGCCCGGACCATAGGAATGT	50119		
Qy	121	ATTACAGTTTGGCCCAAGAACACAAACGTTGGAAACACTCAAGTTTCTTCTCGTATA	180		
Db	50120	ATTACAGTTTGGCCCAAGAACACAAACGTTGGAAACACTCAAGTTTCTTCTCGTATA	50179		
Qy	181	CATCAGCTGGTGTGTCATGCAATGGGACATACCATCTGACGCTTCCCTGTTTCCCTGATT	240		
Db	50180	CATCAGCTGGTGTGTCATGCAATGGGACATACCATCTGACGCTTCCCTGTTTCCCTGATT	50239		
Qy	241	TGTCCTGATGTCTCCCAATACCTCTTTCCCAACCACTCATCTCCCAACCTCACCTTTCTT	300		





Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan  
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction: Helix Research Institute (HRI) (supported by Japan  
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
 HRI, and Biotechnology Center, National Institute of Technology and  
 Evaluation; clone selection for full insert sequencing: HRI and  
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 Matches 143; Conservative 0; Mismatches 6; Indels 2; Gaps 1;  
 238 ATTTGCTGCTGATGTCCTCAATACCTCTTTTCCAAACCACTCATCTCCCACTCTACCTTTT 297  
 1 ATTTGCTGCTGATGTCCTCA--TACCTCTTCCATCCACCTCATCTCCCACTCTACCTTT 58  
 298 CTTTCTTTTGTGTTGCTTTATATATAGTCTGGAGTCTCCCTACAGAGGATACCTTGGCCGG 357  
 59 CTTTCTTTTGTGTTGCTTTATATAGTCTGGAGTCTCCCTACAGAGGATACCTTGGCCGG 118  
 358 GAGTCTCCAGCTACCTTAACCTCAATCCAGG 388  
 119 GAGTCTCCAGCTACCTTAACCTCAATCCAGG 149  
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 LOCUS  
 DEFINITION Sequence 1 from patent US 6492154.  
 ACCESSION AR265350  
 VERSION AR265350.1 GI:29693853  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM  
 Unclassified.  
 1 (bases 1 to 2203)  
 REFERENCE  
 AUTHORS Yan, C., Ketchum, K. A., Di Francesco, V. and Beasley, E. M.  
 TITLE Isolated human kinase proteins, nucleic acid molecules encoding  
 human kinase proteins, and uses thereof  
 JOURNAL Patent: US 6492154-A 1 10-DEC-2002;  
 FEATUERS Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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 Query Match 21.3%; Score 87.4; DB 6; Length 2203;  
 Best Local Similarity 98.9%; Pred. No. 2.1e-15;  
 Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 322 AGTGCTGGAGTCTCCCTACAGAGGATCTTGGCCGGAGTCTCCCAAGTACTCACTTACA 381  
 1061 AGGTGCTGGAGTCTCCCTACAGAGGATCTTGGCCGGAGTCTCCCAAGTACTCACTTACA 1120  
 382 ATCCAGGTAATATTGATCTGAGCTTCTGA 410  
 1121 ATCCAGGTAATATTGATCTGAGCTTCTGA 1149  
 241 TGTCTGATGCTCCCAATACCTCTTTTCCAAACCACTCATCTCCCACTCTACCTTTTCTT 300  
 23336 TGTCTGATGCTCCCA--TACCTCTTCCATCCACCTCATCTCCCACTCTACCTTTTCTT 23279  
 301 TTTCTTTGTTGGCTTTATATAGTCTGGAGTCTCCCTACAGAGGATACCTTGGCCGGAG 360  
 23278 TTTCTTTGTTGGCTTTATATAGTCTGGAGTCTCCCTACAGAGGATACCTTGGCCGGAG 23219  
 361 TCTCAAGCTACCTTAACCTCAATCAGGTAATATTGATCTGAGCTTCTGA 410  
 23218 TCTCAAGCTACCTTAACCTCAATCAGGTAATATTGATCTGAGCTTCTGA 23169  
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 LOCUS  
 DEFINITION Homo sapiens cDNA FLJ34391 f18, clone HCHON2000199.  
 ACCESSION AK091710  
 VERSION AK091710.1 GI:21750145  
 KEYWORDS  
 SOURCE oligo capping; f18 (full insert sequence).  
 ORGANISM Homo sapiens (human)  
 REFERENCE  
 AUTHORS  
 1  
 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,  
 Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,  
 Sekine, M., Ohyashi, M., Nishi, T., Shibahara, T., Tanaka, K.,  
 Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,  
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 Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,  
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 Takeuchi, K., Arita, M., Inose, N., Musashino, K., Yuuki, H., Oshima, A.,  
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 Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,  
 Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,  
 Goto, I., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,  
 Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,  
 Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,  
 Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,  
 Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hiki, T., Kobatake, N.,  
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 Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,  
 Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,  
 Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.  
 Complete sequencing and characterization of 21,243 full-length  
 human cDNAs  
 Nat. Genet. 36 (1), 40-45 (2004)  
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 Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M.,  
 Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K.,  
 Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,  
 Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,  
 Kimura, K., Yanashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,  
 Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,  
 Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,  
 Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.  
 NEDO human cDNA sequencing project  
 Unpublished  
 3 (bases 1 to 2422)  
 Isogai, T. and Yamamoto, J.  
 Direct Submission  
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

```

RESULT 6
AX571873 LOCUS AX571873 2203 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 1 from Patent WO02061060.
ACCESSION AX571873
VERSION AX571873.1 GI:26003999
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Van,C., Ketchum,K., di Francesco,V. and Beasley,E.M.
TITLE Isolated human kinase proteins, nucleic acid molecules encoding
human kinase proteins, and uses thereof
JOURNAL Patent: WO 02061060-A 1 08-AUG-2002;
PE Corporation (NY) (US)
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Query Match 21.3%; Score 87.4; DB 6; Length 2203;
Best Local Similarity 98.9%; Pred. No. 2.1e-15;
Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 322 AGGTCTGGAGTCCCTACAGAGGATACTTGGCCGGAGTCTCCAGGTACCTACTACTACA 381
Db 1061 AGGTCTGGAGTCCCTACAGAGGATACTTGGCCGGAGTCTCCAGGTACCTACTACTACA 1120
Oy 382 ATCCAGGTAATATGATCTGAGCTTCTGA 410
Db 1121 ATCCAGGTAATATGATCTGAGCTTTTGA 1149

RESULT 7
AC132361 LOCUS AC132361 161010 bp DNA linear HTG 03-SEP-2002
DEFINITION Mus musculus chromosome UNK clone RP24-149E13, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
AC132361
VERSION AC132361.1 GI:22657848
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 161010)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 161010)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0149E13
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319

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Consensus quality: 153781 bases at least Q40
Consensus quality: 154797 bases at least Q30
Consensus quality: 155407 bases at least Q20
Insert size: 179000; agarose-fp
Insert size: 159810; sum-of-contigs
Quality coverage: 10.01 in Q20 bases; agarose-fp
Quality coverage: 10.14 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1984: contig of 1984 bp in length
* 1985 2084: gap of unknown length
* 2085 4163: contig of 2079 bp in length
* 4164 4263: gap of unknown length
* 4264 9331: contig of 5068 bp in length
* 9332 9431: gap of unknown length
* 9432 16764: contig of 7333 bp in length
* 16765 16864: gap of unknown length
* 16865 21118: contig of 4254 bp in length
* 21119 21218: gap of unknown length
* 21219 30095: contig of 8877 bp in length
* 30096 30195: gap of unknown length
* 30196 40537: contig of 10342 bp in length
* 40538 40637: gap of unknown length
* 40638 53634: contig of 12997 bp in length
* 53635 53734: gap of unknown length
* 53735 68578: contig of 14844 bp in length
* 68579 68678: gap of unknown length
* 68679 89216: contig of 20538 bp in length
* 89217 89316: gap of unknown length
* 89317 108734: contig of 19418 bp in length
* 108735 108835: gap of unknown length
* 108835 159127: contig of 50293 bp in length
* 159128 159227: gap of unknown length
* 159228 161010: contig of 1783 bp in length.
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293	CCCTTTCCTTTCTGTTGGCTTTATATAGTGCTCGGAGGTCCCTACAGAGGATACATTG	352				
59744	CTTACCCTTTCTTTTTCTTGCTCTGTAAGTTCCTGAGGTCCCTACAGAGGATACCTG	59803				
353	GCCGGGAGTCTCGAAGCTACTCAACTACRATCCAGGTATATT	395				
59804	GCCTGGAGTCTCCAAATGCCCTACTACATCCAGGTACAGTT	59846				

59744 CTTACCTTCTCTCTTCTGTCGGCTGCGTAGGATCCGGAGTGCAGGAGGAAAT  
353 GCCGGAGTCTCCAGTACTTAACCTACATCCAGGTAAATT 395

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	AC116995	linear	DNA	ROD 05-NOV-2003
		173131 bp		
				complete sequence.

DEFINITION	Mus musculus BAC clone library
ACCESSION	AC116995
VERSION	AC116995.3
KEYWORDS	HTG.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Murinae; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 173131)  
Holmes,A., Haglund,K. and Spalding,L.  
AUTHORS  
The sequence of Mus musculus BAC clone RP23-3C16  
TITLE  
Unpublished (2001)  
JOURNAL  
2 (bases 1 to 173131)  
JOURNAL

WILSON, K.  
TITLE Sequencing of *Mus musculus*  
JOURNAL Unpublished (2001)  
REFERENCE 3 (bases 1 to 173131)  
AUTHORS McPherson, J.D. and Waterston, R.H.

**JOURNAL**  
Submitted (05-APR-2002) Genome Sequencing Center,  
Parkway, St. Louis, MO 63108, USA  
4 (bases 1 to 173131)  
McPherson, J. D. and Waterston, R. H.  
**REFERENCE**  
**AUTHORS**

**JOURNAL** Submitted (02-Mar-2002), *Genomics*  
Parkway, St. Louis, MO 63108, USA  
**REFERENCE** 5 (bases 1 to 173131)  
**AUTHORS** McPherson, J.D. and Waterston, R.H.  
**TYPE** Direct Submission

**REFERENCE**  
**AUTHORS**  
**TITLE**  
**ADDRESS**  
**DEPARTMENT OF GENETICS, WASHINGTON**  
**STATE UNIVERSITY**  
**PARKWAY, ST. LOUIS, MO 63108, USA**  
**6 (bases 1 to 173131)**  
**Wilson, R.**  
**Direct Submission**

COMMENT  
On Jul 16, 2002 this sequence version replaced gi:20389753.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC

web site: <http://www.watson.wustl.edu>  
 Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
 ----- Summary Statistics -----  
 Center project name: M\_BA0003C16  
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**NOTICE:** This sequence may not represent the entire sequence of clone sections. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as a double-stranded, sequenced with an alternate all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30).

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RESULT 9  
AC128908  
LOCUS  
DEFINITION Rattus norvegicus clone CH230-320D4, WORKING DRAFT SEQUENCE, 2  
unordered pieces.  
ACCESSION AC128908  
VERSION AC128908.3 GI:25073564  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 179341)  
REFERENCE  
AUTHORS  
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,  
Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,  
Anyalebechi, V., Ayvagi, A., Ayodeji, M., Baca, E., Baden, H.,  
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
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Davila, M. L., Davis, C., Davy-Carroil, L., De Anda, C., Dederich, D.,  
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RESULT 11  
 AK131512 1828 bp mRNA linear PRI 07-MAY-2004  
 Locus Homo sapiens CDNA FLJ16732 fls, clone BNGH42005017, moderately  
 similar to SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 (BC 2.7.1.-).  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS  
 Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R.,  
 Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J.,  
 Isono,Y., Kawai-Hito,Y., Saito,K., Nishikawa,T., Kimura,K.,  
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 Kanda,K., Negatsuma,M., Murakawa,K., Kanehori,K., Negahari,K.,  
 Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S.,  
 Masuho,Y., Nagai,K. and Isogai,T.  
 NEDO human cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 1828)  
 Isogai,T. and Yamamoto,J.  
 Direct Submission  
 Submitted (01-MAR-2004) Takao Isogai, FLJ Project (HRI Team); 2-6-7  
 Karusa-Kamatari, Kisarazu, Chiba 292-0819, Japan  
 (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 COMMENT  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; CDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction: Helix Research Institute (HRI) (supported by Japan  
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
 HRI, and Biotechnology Center, National Institute of Technology and  
 Evaluation; clone selection for full insert sequencing: HRI and  
 RAB; annotation: HRI and RAB.  
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QY 322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381  
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QY 382 ATCCAG 387  
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Db 285 ATCCAG 290

RESULT 14  
AR236733  
LOCUS AR236733 481 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 14 from patent US 6465232.  
ACCESSION AR236733  
VERSION AR236733.1 GI:27280884  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 481)  
TITLE Robison,K.E.  
Nucleic acid molecules encoding human kinase and phosphatase  
homologues and uses therefor  
JOURNAL Patent: US 6465232-A 14 15-OCT-2002;  
FEATURES Location/Qualifiers  
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## ORIGIN

Query Match 16.1%; Score 66; DB 6; Length 481;  
Best Local Similarity 100.0%; Pred. No. 7e-09;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381  
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Db 285 ATCCAG 290

RESULT 15  
AX056403  
LOCUS AX056403 1077 bp DNA linear PAT 13-JAN-2001  
DEFINITION Sequence 47 from Patent WO0073469.  
ACCESSION AX056403  
VERSION AX056403.1 GI:12229110  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Plowman,G.D., Martinez,R., Whyte,D. and Sudersanam,S.  
TITLE Protein kinases  
JOURNAL Patent: WO 0073469-A 47 07-DEC-2000;  
Sugen, Inc. (US)

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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5314.229 Million cell updates/sec

Title: US-10-786-065-3\_COPY\_50000\_50409

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Sequence: 1 atgatcatgataatcatgcag.....attatgatctgagcttctga 410

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	410	100.0	5332	6 AAL48890 Human pft
2	87.4	21.3	2203	6 AAL48889 Human pft
3	68	16.6	1828	12 ADM16422 DNA encod
4	67	16.3	888	10 ABZ77160 Human pro
5	66	16.1	481	6 AAG17061 Human pro
6	66	16.1	481	10 RAD61613 Human pro
7	66	16.1	481	10 ABX14985 Human pro
8	66	16.1	1077	4 AAF44668 Human pft
9	66	16.1	1077	12 ADI29366 Human pft
10	66	16.1	1308	6 AAL48891 Human pft
11	66	16.1	1308	9 ACC79970 Human ser
12	66	16.1	1311	10 ADC30755 Human nov
13	66	16.1	1376	8 ABA00722 Human xpp
14	66	16.1	1534	9 ACC79969 Human ser
15	66	16.1	1534	9 ACC79967 Human ser
16	66	16.1	1584	9 ACC79968 Human ser
17	66	16.1	1628	9 ACC79971 Human ser
18	66	16.1	2140	11 ADL22554 Human dis
19	66	16.1	2250	12 ADJ96563 Human cyc
20	40.4	9.9	189013	8 ACf62741 Cancer ba
21	40.4	9.9	189013	8 ADB20856 MRP1 base

22	40.4	9.9	189013	10	ADB87945	Adh87945 Human UGT
23	40.4	9.9	189013	10	ADB96928	Adb96928 Human MDR
24	40.4	9.9	189013	10	ADB92119	Adb92119 Human MDR
25	38.2	9.3	113515	6	ABL34175	Abi34175 Human imm
26	37	9.0	9774	5	ABA19485	Abai19485 Human ner
27	36.4	8.9	382	4	AAI87526	Aai87526 Human pol
28	36.2	8.8	2259	11	ADM01612	Adm01612 Human cdn
29	36.2	8.8	50000	10	ADC60733	Adc60733 Human sll
30	36	8.8	2703	4	ABL20823	Abi20823 Drosophil
31	36	8.8	2921	4	ABL02065	Abi02065 Drosophil
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36	35.8	8.7	110000	6	ABT00010_08	Continuation (9 of
37	35.8	8.7	110000	6	ABT01503_08	Continuation (9 of
38	35.8	8.7	110000	12	ADH77485_08	Continuation (9 of
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42	35	8.5	405	4	AAK98075	AAK98075 Human neu
43	35	8.5	405	6	ABT01352	Abt01352 Human neu
44	35	8.5	405	6	ABT02845	Abt02845 Human neu
45	35	8.5	405	12	ADH77607	Adh77607 Human neu

#### ALIGNMENTS

##### RESULT 1

AAL48890  
ID AAL48890 standard; DNA; 53332 BP.

XX AC AAL48890;

XX DT 24-OCT-2002 (first entry)

XX DE Human Pftaire family kinase gene.

XX KW Human; Pftaire family kinase; kinase; enzyme; testis; brain; cytosstatic;  
XX KW uterus endometrium adenocarcinoma; lung fibroblast; splice form;  
XX KW kidney renal cell adenocarcinoma; gene therapy; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT variation replace(864,T)

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FT variation replace(2111,G)

FT CDS /tag= b

FT CDS 2118..50409

FT /tag= c

FT /product= "kinase"

FT /note= "this sequence contains introns"

FT exon 2118..2240

FT /tag= d

FT intron 2241..2946

FT /tag= e

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FT exon 2947..3096

FT /tag= f

FT /number= 2

FT intron 3097..3310

FT /tag= g

FT /number= 2

FT variation replace(3259,C)

FT /tag= h

FT exon 3311..3405

FT /tag= i

FT /number= 3

FT intron 3406..7938

FT /tag= j



AC AAL4889;  
 XX 24-OCT-2002 (first entry)  
 DE Human Pftaire family kinase splice form 1 coding sequence.  
 XX Human; Pftaire family kinase; kinase; enzyme; testis; brain; cytosstatic;  
 KW uterus endometrium adenocarcinoma; lung fibroblast; splice form;  
 KW kidney renal cell adenocarcinoma; gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
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 FT /\*tag= a  
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 FT /\*tag= b  
 FT /\*product= "kinase"  
 FT 3'UTR 1149..2203  
 FT /\*tag= c  
 XX  
 PN WO200261060-A2.  
 XX  
 XX 08-AUG-2002.  
 XX  
 XX 17-JAN-2002; 2002WO-US001106.  
 XX  
 XX 31-JAN-2001; 2001US-0265151P.  
 PR 09-MAR-2001; 2001US-00801861.  
 XX  
 XX (PEKE ) PE CORP NY.  
 XX  
 XX Yan C, Ketchum K, Di Francesco V, Beasley EM;  
 XX WPI; 2002-608515/65.  
 DR P-PSDB; AAO18613.  
 XX  
 XX New human kinase peptide and nucleic acid molecule, useful for treating  
 PT disorders associated with abnormal expression of kinase protein, e.g.  
 PT adenocarcinoma of uterus or lung, in drug screening assays and  
 PT pharmacogenomic analysis.  
 XX  
 XX Claim 4; Fig 1; 131pp; English.  
 XX  
 CC The present invention provides the protein, cDNA and gene sequences of  
 CC two splice variants of a human Pftaire family kinase. The sequences are  
 CC specifically expressed in the human testis, brain, uterus endometrium  
 CC adenocarcinomas, lung fibroblasts, kidney renal cell adenocarcinomas, and  
 CC can be used to treat related diseases. The present sequence is the cDNA  
 CC of splice variant 1 of the invention  
 XX  
 SQ Sequence 2203 BP; 657 A; 460 C; 538 G; 548 T; 0 U; 0 Other;  
 Query Match 21.3%; Score 87.4; DB 6; Length 2203;  
 Best Local Similarity 98.9%; Pred. No. 1.3e-17;  
 Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 322 AGGTCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTACTACA 381  
 Db |||||  
 Db 1061 AGGTCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTACTACA 1120  
 QY 382 ATCCAGGTAATATTGATCTGAGCTTCTGA 410  
 Db |||||  
 Db 1121 ATCCAGGTAATATTGATCTGAGCTTCTGA 1149  
 RESULT 3  
 ADM16422  
 ID ADM16422 standard; DNA; 1828 BP.  
 XX  
 AC ADM16422;  
 XX  
 DT 17-JUN-2004 (first entry)

XX DNA encoding human kinase protein, seq id 1.  
 DE  
 XX Cytostatic; cardiant; neuroprotective; nootropic; antiinfertility;  
 KW vulnery; antidiabetic; kinase; cancer; heart disease;  
 KW Alzheimer's disease; infertility; wound; diabetes; neurological disease;  
 KW gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 87..1124  
 FT /\*tag= a  
 FT /\*product= "kinase"  
 XX  
 PN WO2004024913-A1.  
 XX  
 XX 25-MAR-2004.  
 PD  
 XX 10-SEP-2003; 2003WO-JP011552.  
 PF  
 XX 10-SEP-2002; 2002JP-00264345.  
 PR  
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
 PA (ZOE-) ZOEGENE CORP.  
 XX  
 XX Kondo J, Kawai K, Miyama N, Nakajima M, Isogai T, Sugiyama T;  
 PI Wakamatsu A, Irie R, Ishii S;  
 XX WPI; 2004-270042/25.  
 DR P-PSDB; ADM16427.  
 XX  
 XX Proteins of human origin having kinase activity, useful for prevention  
 PT and treatment of kinase-associated diseases including cancer, heart  
 PT disease and Alzheimer's disease.  
 XX  
 XX Claim 4; SEQ ID NO 1; 105pp; Japanese.  
 XX  
 CC The invention relates to four proteins of human origin (I) having kinase  
 CC activity, and to proteins derived from these by addition, deletion and/or  
 CC substitution of one or more amino acid residues, and having similar  
 CC activity. The proteins and other aspects of the invention are useful for  
 CC the prevention and treatment of kinase-associated diseases including  
 CC cancer, heart disease, Alzheimer's disease, infertility, wounds, diabetes  
 CC and neurological diseases. The current sequence represents a human DNA  
 CC encoding a protein having kinase activity.  
 XX  
 SQ Sequence 1828 BP; 496 A; 398 C; 450 G; 484 T; 0 U; 0 Other;  
 Query Match 16.6%; Score 68; DB 12; Length 1828;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 322 AGGTCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTACTACA 381  
 Db |||||  
 Db 967 AGGTCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTACTACA 1026  
 QY 382 ATCCAGGT 389  
 Db |||||  
 Db 1027 ATCCAGGT 1034  
 RESULT 4  
 ABZ77160  
 ID ABZ77160 standard; cDNA; 888 BP.  
 XX  
 AC ABZ77160;  
 XX  
 XX 07-MAY-2003 (first entry)  
 DT  
 XX Human protein kinase encoding cDNA SEQ ID NO:69.  
 DE  
 XX Human; protein kinase; enzyme; antiasthmatic; antiinflammatory;

Thu Jan 13 09:56:04 2005

antidiabetic; antiparkinsonian; antimigraine; cardiant; cytostatic; immunosuppressive; vulnery; gene therapy; COPD; asthma; migraine; chronic obstructive pulmonary disease; non-insulin dependent diabetes; Parkinson's disease; myocardial infarction; inflammatory bowel disease; autoimmune disorder; allograft rejection; graft versus host disease; cancer; leukaemia; wound granulation; gene; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 1..888  
/tag= a  
/partial  
/product= "protein kinase"  
/note= "no start or stop codons given"

WO2003000901-A2.

03-JAN-2003.

24-JUN-2002; 2002WO-IB002358.

26-JUN-2001; 2001US-0301098P.

06-NOV-2001; 2001US-032870P.

(DECO-) DECODE GENETICS EHF.

Martinez RAM, Sigurdson GT;  
WPI; 2003-201429/19.

P-PSDB; ABP96082.

New protein kinase genes and polypeptides, useful for diagnosing diseases associated with a protein kinase, or in gene therapy for treating e.g. Parkinson's disease, migraine, myocardial infarction, allograft rejection or cancers.

Claim 1; Page 85; 258pp; English.

AB277126 to AB277165 encode the human protein kinases given in ABP96048 to ABP96087. The protein kinases have antiasthmatic, antiinflammatory, antidiabetic, antiparkinsonian, antimigraine, cardiant, cytostatic, immunosuppressive and vulnery activities, and can be used in gene therapy. A protein kinase therapeutic agent from the present invention, particularly a protein kinase gene agonist or antagonist, can be used for treating a disease or condition associated with a protein kinase in an individual. These diseases include chronic obstructive pulmonary diseases (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease, migraine, myocardial infarction, inflammatory bowel disease, autoimmune disorders (e.g. allograft rejection or graft vs. host disease), cancers (e.g. leukaemias) or wound granulation

Sequence 888 BP; 214 A; 234 C; 207 G; 233 T; 0 U; 0 Other;  
Query Match 16.3%; Score 67; DB 10; Length 888;  
Best Local Similarity 100.0%; Pred. No. 4.2e-11;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGTACTACTACTACA 381  
647 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGTACTACTACTACA 706  
382 ATCCAGG 388  
707 ATCCAGG 713

RESULT 5  
AAS17061  
ID AAS17061 standard; cDNA; 481 BP.  
XX  
AC AAS17061;  
XX

14-FEB-2002 (first entry)

Human protein kinase cDNA mine42958human\_c1.

Human; ss; protein kinase; mine42958human\_c1; cytostatic; antianginal; hypotensive; cardiant; cardiovascular disorder; heart failure; hypertension; atrial fibrillation; dilated cardiomyopathy; cancer; idiopathic cardiomyopathy; angina; proliferative disorder; cancer; melanoma; prostate cancer; cervical cancer; breast cancer; colon sarcoma; gene therapy.

Homo sapiens.

US6309849-B1.

30-OCT-2001.

31-AUG-1999; 99US-00387212.

31-AUG-1999; 99US-00387212.

(MILL-) MILLENNIUM PHARM INC.

Robison KE;  
WPI; 2002-048371/06.

Identifying compound which binds to a Kinase, useful for treating diseases e.g. cancer, by contacting kinase with test compound and detecting its binding to the kinase.

Example 1; Fig 14; 45pp; English.

The invention relates to identifying a compound which binds to a Kinase (encoded by a nucleotide sequence of 1868, 403, 545, 361, 473, 3001, 526, 683 or 1448 base pair (bp) as given in the specification) comprising for contacting the kinase with a test compound under suitable conditions for binding, and detecting binding of the compound to the kinase. The method is useful for identifying a compound which binds to the kinase. The method for isolating compounds which modify the activity of the kinase. The identified compounds are useful for treating a subject having a disorder characterised by aberrant kinase activity where the disorder includes cellular growth related disorders which includes a disorder, disease, or condition characterised by a deregulation, e.g. an upregulation or a downregulation, of cellular growth. Cellular growth deregulation due to deregulation of cellular proliferation, cell cycle progression, cellular differentiation and/or cellular hypertrophy, cardiovascular disorders such as heart failure, hypertension, atrial fibrillation, dilated cardiomyopathy, idiopathic cardiomyopathy, or anginal, proliferative disorders such as cancer (including melanoma, prostate cancer, cervical, breast, colon sarcoma). The kinases and antibodies raised against them are useful in one or more method such as screening assays, predictive medicine and methods of treatment. The nucleic acid molecules are useful for expressing kinase and phosphatase protein (e.g. in gene therapy applications), to detect kinase and phosphatase mRNA or a genetic alteration in a kinase and phosphatase gene and to modulate kinase and phosphatase activity. The present sequence is a cDNA for a human protein kinase

Sequence 481 BP; 100 A; 136 C; 123 G; 122 T; 0 U; 0 Other;  
Query Match 16.1%; Score 66; DB 6; Length 481;  
Best Local Similarity 100.0%; Pred. No. 6.7e-11;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGTACTACTACA 381  
225 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGTACTACTACA 284  
382 ATCCAG 387  
285 ATCCAG 290



## RESULT 6

AA061613  
ID AAD61613 standard; cDNA; 481 BP.  
XX  
AC AAD61613;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human protein kinase cDNA, 42958S1.  
XX  
KW Kinase; phosphatase; drug target; therapy; gene; human; ss.  
XX  
OS Homo sapiens.  
XX  
US2003104505-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 12-APR-2002; 2002US-00121925.  
XX  
PR 31-AUG-1999; 99US-00387212.  
XX  
PR 07-SEP-2001; 2001US-00948802.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Robison KE;  
XX  
DR WPI; 2003-801234/75.  
XX

XX Detecting and modulating the activity of specified kinases and  
XX phosphatases which are potentially useful as drug targets.  
XX  
XX Claim 1; Fig 14; Opp; English.  
XX  
XX The present invention relates to a method for detecting the presence of a  
XX kinases or phosphatases encoded by nucleotides. The kinases and  
XX phosphatases and their encoding nucleic acids are potentially useful as  
XX drug targets. The present invention may also be useful in diagnosing  
XX disease. The present sequence is human protein kinase cDNA  
XX  
XX Sequence 481 BP; 100 A; 136 C; 123 G; 122 T; 0 U; 0 Other;  
XX  
XX Query Match 16.1%; Score 66; DB 10; Length 481;  
XX Best Local Similarity 100.0%; Pred. No. 6.7e-11;  
XX Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 322 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACCTAACTACA 381  
XX |||||  
XX 225 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACCTAACTACA 284  
XX  
XX 382 ATCCAG 387  
XX |||||  
XX 285 ATCCAG 290  
XX

## RESULT 7

ABX14985  
ID ABX14985 standard; cDNA; 481 BP.  
XX  
AC ABX14985;  
XX  
DT 13-MAR-2003 (first entry)  
XX  
DE Human protein kinase cDNA mine42958human\_s1.  
XX

XX Human; ss; protein kinase; mine42958human\_s1; cancer; cytostatic;  
XX antiangiinal; hypotensive; cardiant. proliferative disorder;  
XX cellular growth related disorder; cardiovascular disorder; heart failure;  
XX hypertension; atrial fibrillation; dilated cardiomyopathy;  
XX idiopathic cardiomyopathy; angina.  
XX  
XX Homo sapiens.  
OS

XX

PN US6465232-B1.

XX

PD 15-OCT-2002.

XX

PF 07-SEP-2001; 2001US-00948802.

XX

PR 31-AUG-1999; 99US-00387212.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Robison KE;

XX

WPI; 2003-147067/14.

XX

XX Novel human kinase and phosphatase nucleic acid molecules useful for  
XX treating cellular proliferative disorders such as cancer, cardiovascular  
XX diseases, hypertension, heart failure and angina.

XX Example 1; Fig 14; 47pp; English.

XX

XX The invention relates to an isolated human kinase and phosphatase nucleic  
XX acid molecule appearing as ABX14972, ABX14973, ABX14975, ABX14976, and  
XX ABX14978-ABX14981, or their complement. Also included are: (1) an  
XX isolated nucleic acid molecule which is at least 90 % identical to the  
XX nucleotide sequence ABX14973 or ABX14975, or 95 % identical to the  
XX complement, where the nucleic acid molecule encodes a polypeptide having  
XX a kinase activity; (2) An isolated nucleic acid molecule which hybridizes  
XX to ABX14973, ABX14975, ABX14976, and ABX14978 in 6X saline sodium citrate  
XX (SSC) at 45 plusOC, followed by one or more washes in 0.2X SSC, 0.1%  
XX sodium dodecyl sulphate (SDS) at 65 plusOC, where the molecule encodes a  
XX polynucleotide with kinase activity; (3) a vector comprising the  
XX and (4) expressing a polypeptide by culturing a host cell comprising the  
XX The nucleic acids are useful as modulating agents in regulating a variety  
XX of cellular processes, and fragments are useful as primers or  
XX hybridisation probes for detecting kinase and phosphatase encoding  
XX nucleic acids. The nucleic acids are useful for treating proliferative  
XX disorders such as cancer and cellular growth related disorders including  
XX cardiovascular disorders such as heart failure, hypertension, atrial  
XX fibrillation, dilated cardiomyopathy, idiopathic cardiomyopathy or  
XX angina. The present sequence is one of the human kinase or phosphatase  
XX cDNAs of the invention

XX Sequence 481 BP; 100 A; 136 C; 123 G; 122 T; 0 U; 0 Other;

XX Query Match 16.1%; Score 66; DB 10; Length 481;

XX Best Local Similarity 100.0%; Pred. No. 6.7e-11;

XX Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACCTAACTACA 381

DB |||||

DB 225 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACCTAACTACA 284

QY 382 ATCCAG 387

DB |||||

DB 285 ATCCAG 290

## RESULT 8

AAF44668

ID AAF44668 standard; cDNA; 1077 BP.

XX

AC AAF44668;

XX

DT 27-MAR-2001 (first entry)

XX

DE Novel protein kinase cDNA, SEQ ID NO: 48.

XX

KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;  
KW immunosuppressive; cardiant; renal; antiinflammatory; antiaethmatic;

US-10-786-065-3\_copy\_50000\_50409\_rmg

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Alzheimer's disease; neurodegenerative disorder; hyperproliferative disorder; cytostatic.

Homo sapiens.  
US2003232771-A1.

18-DEC-2003.

17-JUN-2002; 2002US-00174319.

17-JUN-2002; 2002US-00174319.

(ISIS-) ISIS PHARM INC.

Ward DT, Freier SM, Dobie KW;

WPI; 2004-052188/05.

P-PSDB; ADI29248.

New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3); useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.

Disclosure; Fig 2; 233pp; English.

The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3); that specifically hybridizes with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated cDNA included in the figures but not mentioned anywhere else in the specification.

Sequence 1077 BP; 269 A; 257 C; 248 G; 303 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 12; Length 1077;

Best Local Similarity 100.0%; Pred. No. 9.6e-11; Indels 0; Gaps 0; Matches 66; Conservative 0; Mismatches 0;

322 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACCTACTACA 381  
437 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACCTACTACA 496

382 ATCCAG 387

497 ATCCAG 502

RESULT 10

ADL48891

ID AAL48891 standard; cDNA; 1308 BP.

XX AAL48891;

XX 24-OCT-2002 (first entry)

Human Pftaire family kinase splice form 2 coding sequence.

Human; Pftaire family kinase; kinase; enzyme; testis; brain; cytostatic;

uterus endometrium adenocarcinoma; lung fibroblast; splice form;

kidney renal cell adenocarcinoma; gene therapy; gene; ss.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

Homo sapiens.

WO200073469-A2.

07-DEC-2000.

26-MAY-2000; 2000WO-US014842.

28-MAY-1999; 99US-0136503P.

(SUGR-) SUGEN INC.

Plowman GD, Martinez R, Whyte D, Sudersanam S;

WPI; 2001-032161/04.

P-PSDB; AAB65641.

Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.

Example 1; Fig 2; 310pp; English.

The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders

Sequence 1077 BP; 269 A; 257 C; 248 G; 303 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 4; Length 1077;

Best Local Similarity 100.0%; Pred. No. 9.6e-11;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACCTACTACA 381  
437 AGGTGCTGGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAGCTACCTACTACA 496

382 ATCCAG 387

497 ATCCAG 502

RESULT 9

ADL29366

ID ADL29366 standard; cDNA; 1077 BP.

XX ADL29366;

XX 22-APR-2004 (first entry)

Human MARK3-associated cDNA #36.

Human; ss; antisense gene therapy; MARK3;

MAP/microtubule affinity-regulating kinase 3; cancer;

```
FT CDS 1..1306
FT /*tag= a
FT /product= "kinase"
XX
XX WO200261060-A2.
XX
XX 08-AUG-2002.
XX
XX 17-JAN-2002; 2002WO-US001106.
XX
XX 31-JAN-2001; 2001US-0265151P.
XX
XX 09-MAR-2001; 2001US-00801861.
XX
XX (PEKE ) PE CORP NY.
XX
XX Yan C, Ketchum K, Di Francesco V, Beasley EM;
XX WPI; 2002-608515/65.
XX P-PSDB; AA018614.
XX
XX New human kinase peptide and nucleic acid molecule, useful for treating
XX PT disorders associated with abnormal expression of kinase protein, e.g.
XX PT adenocarcinoma of uterus or lung, in drug screening assays and
XX PT pharmacogenomic analysis.
XX
XX Claim 4; Fig 1; 131pp; English.
XX
XX The present invention provides the protein, cDNA and gene sequences of
XX CC two splice variants of a human Pffaire family kinase. The sequences are
XX CC specifically expressed in the human testis, brain, uterus endometrium
XX CC adenocarcinomas, lung fibroblasts, kidney renal cell adenocarcinomas, and
XX CC can be used to treat related diseases. The present sequence is the cDNA
XX CC of splice variant 2 of the invention
XX
XX Sequence 1308 BP; 328 A; 332 C; 330 G; 318 T; 0 U; 0 Other;
XX
XX Query Match 16.1%; Score 66; DB 6; Length 1308;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-10;
XX Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 322 AGGTGCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGTACCTAACTACA 381
XX 944 AGGTGCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGTACCTAACTACA 1003
XX
XX 382 ATCCAG 387
XX 1004 ATCCAG 1009
XX
XX RESULT 11
XX ACC79970
XX ID ACC79970 standard; cDNA; 1308 BP.
XX
XX AC ACC79970;
XX
XX 09-SEP-2003 (first entry)
XX
XX Human serine/threonine protein kinase encoding cDNA SEQ ID NO:8.
XX
XX Human; serine/threonine protein kinase; kinase; enzyme; cytotostatic;
XX KW antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic;
XX KW cerebrotective; antiinflammatory; gastrointestinal; hepatotropic;
XX KW gynaecological; uropathic; dermatological; gene therapy; cancer;
XX KW diabetes; central nervous system disorder; CNS disorder; liver disease;
XX KW respiratory disorder; chronic obstructive pulmonary disease; stroke;
XX KW cardiovascular disorder; dermatological disorder; urological disorder;
XX KW gastrointestinal disease; haematological disorder; Alzheimer's disease;
XX KW musculoskeletal disorder; reproductive disorder; Parkinson's disease;
XX KW neuropathic pain; gene; ss.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
XX Key
```

```
FT CDS 1..1308
FT /*tag= a
FT /product= "serine/threonine protein kinase"
XX
XX WO2003046167-A1.
XX
XX 05-JUN-2003.
XX
XX 26-NOV-2002; 2002WO-EP013268.
XX
XX 27-NOV-2001; 2001US-0333131P.
XX
XX (FARB ) BAYER AG.
XX
XX Koehler RH;
XX
XX WPI; 2003-505196/47.
XX P-PSDB; ABR57361.
XX
XX New polynucleotide encoding a serine/threonine protein kinase
XX PT polypeptide, useful for diagnosing, preventing or treating diseases
XX PT associated with serine/threonine protein kinase dysfunction, e.g. cancer
XX PT or diabetes.
XX
XX Disclosure; Fig 8; 196pp; English.
XX
XX The present sequence encodes a human serine/threonine protein kinase (I).
XX CC (I) has cytostatic, antidiabetic, neuroprotective, antiparkinsonian,
XX CC nootropic, cerebrotective, analgesic, antiinflammatory, hepatotropic,
XX CC gastrointestinal, gynaecological, uropathic and dermatological
XX CC activities, and can be used in gene therapy. Serine/threonine protein
XX CC kinase polynucleotide and polypeptide sequences can be used in
XX CC diagnosing, preventing, ameliorating or treating diseases associated with
XX CC serine/threonine protein kinase dysfunction. They may also be used to
XX CC identify test compounds that may act, for example, as activators or
XX CC inhibitors at the enzyme's active site. The human serine/threonine
XX CC protein kinase and its fragments are also useful in raising specific
XX CC antibodies that can block the enzyme and effectively reduce its activity.
XX CC Human serine/threonine protein kinase sequences can be used in the
XX CC preparation of a medicament for modulating the activity of a serine/
XX CC threonine protein kinase in a disease, e.g. cancer, diabetes, a central
XX CC nervous system (CNS) disorder, a respiratory disorder (including chronic
XX CC obstructive pulmonary disease), a cardiovascular disorder, a
XX CC dermatological disorder, a gastrointestinal or liver disease, a
XX CC haematological disorder, a musculoskeletal disorder, a reproductive
XX CC disorder, or a urological disorder. CNS disorders may include Alzheimer's
XX CC disease, Parkinson's disease, stroke or neuropathic pain
XX
XX Sequence 1308 BP; 328 A; 332 C; 330 G; 318 T; 0 U; 0 Other;
XX
XX Query Match 16.1%; Score 66; DB 9; Length 1308;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-10;
XX Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 322 AGGTGCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGTACCTAACTACA 381
XX 944 AGGTGCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGTACCTAACTACA 1003
XX
XX 382 ATCCAG 387
XX 1004 ATCCAG 1009
XX
XX RESULT 12
XX ADC30755
XX ID ADC30755 standard; cDNA; 1311 BP.
XX
XX AC ADC30755;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human novel cDNA sequence, SEQ ID NO:837.
XX
XX
```

Human; diagnostic; drug screening; forensics; gene mapping;  
biodiversity assessment; Parkinson's disease; Alzheimer's disease;  
neurodegenerative diseases; anaemia; platelet disorder; wound; burns;  
ulcers; osteoporosis; autoimmune disease; cancer;  
molecular weight marker; food supplement; antiparkinsonian; nootropic;  
neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;  
antitumor; osteopathic; immunosuppressive; antiinflammatory; cytostatic;  
gene therapy; gene; ss.  
Homo sapiens.  
WO2003029271-A2.  
10-APR-2003.  
24-SEP-2002; 2002WO-US030474.  
24-SEP-2001; 2001US-0324631P.  
(HYSE-) HYSEQ INC.  
Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;  
Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;  
Haley-Vicente D, Drmanac RT;  
WPI; 2003-371981/35.  
P-PSDB; ADC31726.  
New polynucleotide and polypeptide useful for diagnosing, preventing or  
treating conditions such as neurodegenerative diseases, anemias, platelet  
disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
cancer.  
Claim 1; SEQ ID NO 837; 1185pp; English.  
The invention relates to 971 novel human cDNA sequences (ADC29919-  
ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The  
invention also relates to nucleic acid sequences over 99% identical with  
the novel human cDNAs. The invention additionally encompasses expression  
vectors and host cells comprising a nucleic acid of the invention; the  
recombinant production of a polypeptide of the invention; an antibody  
against a polypeptide of the invention; a method of detecting  
polynucleotides or polypeptides of the invention; and methods of  
identifying a compound which binds to a polypeptide of the invention. The  
invention further discloses methods of preventing, treating or  
ameliorating a medical condition; kits comprising polynucleotide probes  
and/or monoclonal antibodies for carrying out the methods of the  
invention; methods for the identification of compounds that modulate the  
expression or activity of the polynucleotide and/or polypeptide; and 767  
contig sequences corresponding to the cDNA sequences of the invention  
(ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628  
-ADC33394). The nucleic acids and polypeptides of the invention, in the  
useful in diagnostics, drug screening, forensics, gene mapping, in the  
identification of mutations responsible for genetic disorders or other  
traits, for assessing biodiversity, and in producing many other types of  
data and products dependent on DNA and amino acid sequences. They are  
also used for treating diseases such as Parkinson's disease, Alzheimer's  
disease and other neurodegenerative diseases, anaemia, platelet  
disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
cancer. The nucleic acids may also be used as hybridisation probes or  
primers, and in the recombinant production of a protein. The polypeptides  
are also useful in generating antibodies, as molecular weight markers,  
and as food supplements. The present sequence represents a specifically  
claimed human cDNA sequence of the invention. Note: The sequence data for  
this patent did not form part of the printed specification, but was  
obtained in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 1311 BP; 332 A; 328 C; 329 G; 322 T; 0 U; 0 Other;  
Query Match 16.1%; Score 66; DB 10; Length 1311;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGTGCTGGGAGTCCCTACAGAGTACTTGGCGGGAGTCTCCAAAGCTACCTAATACTACA 381  
893 AGGTGCTGGGAGTCCCTACAGAGTACTTGGCGGGAGTCTCCAAAGCTACCTAATACTACA 952  
382 ATCCAG 387  
953 ATCCAG 958  
RESULT 13  
ABAO0722  
ID ABA00722 standard; cDNA; 1376 BP.  
XX  
AC ABA00722;  
XX  
DT 04-MAR-2003 (first entry)  
XX  
DE Human KPP-7 cDNA, Incyte ID No. 7494145CB1.  
XX  
KW Gene; kinase; phosphatase; KPP; cell proliferation; arterionclerosis;  
atherosclerosis; cirrhosis; hepatitis; reproduction; infertility;  
paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis;  
primary thrombocytopaenia; cancer; development; renal tubular acidosis;  
anaemia; mental retardation; neurological disorder; Alzheimer's disease;  
Parkinson's disease; epilepsy; Sjogren's syndrome; rheumatoid arthritis; AIDS;  
menstrual cycle; autoimmune; inflammation; Crohn's disease; allergy;  
autoimmune thyroiditis; contact dermatitis; Goodpasture's syndrome; gout;  
diabetes mellitus; glomerulonephritis; contact dermatitis; Crohn's disease; allergy;  
Graves' disease; Hashimoto's thyroiditis; irritable bowel syndrome;  
multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;  
Reiter's syndrome; mouse; PPTARE kinase; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 298..1263  
FT FT /\*tag= a "KPP-7"  
XX  
PN WO200290530-A2.  
XX  
PD 14-NOV-2002.  
XX  
PF 16-JAN-2002; 2002WO-US001369.  
XX  
PR 18-JAN-2001; 2001US-0263083P.  
PR 23-FEB-2001; 2001US-0271117P.  
PR 23-FEB-2001; 2001US-0271205P.  
PR 16-MAR-2001; 2001US-0276859P.  
PR 23-MAR-2001; 2001US-0278504P.  
PR 23-MAR-2001; 2001US-0278522P.  
PR 29-MAR-2001; 2001US-0280266P.  
PR 29-MAR-2001; 2001US-0280510P.  
XX  
PA (INCV-) INCYTE GENOMICS INC.  
XX  
PI Lee EA, Wallia NK, Baughn MR, Ison CH, Gururajan R, Arvizu C;  
PI Yao MG, Jackson JL, Tang TY, Yue H, Tran B, Ding L, Lu DAM;  
PI Lal PG, Warren BA;  
XX  
XX WPI; 2003-111972/10.  
XX P-PSDB; AAG79729.  
XX  
XX New human kinases and phosphatases and polynucleotides, useful for  
diagnosing, treating or preventing autoimmune or inflammatory disorders  
(e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
cancer or hepatitis.  
XX  
PS Claim 5; Page 144; 144pp; English.  
XX  
XX The sequences given in ABA00716-23 encode human kinases and phosphatases  
CC (KPP). The KPP polypeptides, polynucleotides, and agonists and  
CC

antagonists to them, are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of proteins associated with KPP. The protein encoded by this sequence is homologous to mouse PPTAIRE kinase

Sequence 1376 BP; 374 A; 321 C; 342 G; 339 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 8; Length 1376;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGGTCTGGAGTCTCCTACAGAGGATACCTTGGCCGGAGTCTCCAGTACTTAATACTACA 381  
|||||  
1088 AGGTCTGGAGTCTCCTACAGAGGATACCTTGGCCGGAGTCTCCAGTACTTAATACTACA 1147  
|||||

382 ATCCAG 387  
|||||

1148 ATCCAG 1153  
|||||

# RESULT 14

ACCT79969  
ID ACC79969 standard; cDNA; 1534 BP.

ACCT79969;

09-SEP-2003 (first entry)

Human serine/threonine protein kinase nucleotide sequence SEQ ID NO:5.

Human; serine/threonine protein kinase; kinase; enzyme; cytostatic; antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic; cerebrotective; antiinflammatory; gastrointestinal; hepatotropic; gynaecological; uropathic; dermatological; gene therapy; cancer; diabetes; central nervous system disorder; CNS disorder; liver disease; respiratory disorder; chronic obstructive pulmonary disease; stroke; cardiovascular disorder; dermatological disorder; urological disorder; gastrointestinal disease; haematological disorder; Alzheimer's disease; musculoskeletal disorder; reproductive disorder; Parkinson's disease; neuropathic pain; gene; ss.

Homo sapiens.

WO2003046167-A1.

05-JUN-2003.

26-NOV-2002; 2002WO-EP013268.

27-NOV-2001; 2001US-0333131P.

(FARB ) BAYER AG.

Koehler RH;

WPI; 2003-505196/47.

New polynucleotide encoding a serine/threonine protein kinase

PT polypeptide, useful for diagnosing, preventing or treating diseases associated with serine/threonine protein kinase dysfunction, e.g. cancer or diabetes.

Disclosure; Fig 5; 196pp; English.

The present sequence represents a human serine/threonine protein kinase (I) related nucleotide sequence from the present invention. (i) has cytostatic, antidiabetic, neuroprotective, antiparkinsonian, nootropic, cerebrotective, analgesic, antiinflammatory, hepatotropic, gastrointestinal, gynaecological, uropathic and dermatological activities, and can be used in gene therapy. Serine/threonine protein kinase polynucleotide and polypeptide sequences can be used in diagnosing, preventing, ameliorating or treating diseases associated with serine/threonine protein kinase dysfunction. They may also be used to identify test compounds that may act, for example, as activators or inhibitors at the enzyme's active site. The human serine/threonine protein kinase and its fragments are also useful in raising specific antibodies that can block the enzyme and effectively reduce its activity. Human serine/threonine protein kinase sequences can be used in the preparation of a medicament for modulating the activity of a serine/threonine protein kinase in a disease, e.g. cancer, diabetes, a central nervous system (CNS) disorder, a respiratory disorder (including chronic obstructive pulmonary disease), a cardiovascular disorder, a dermatological disorder, a gastrointestinal or liver disease, a haematological disorder, a musculoskeletal disorder, a reproductive disorder, or a urological disorder. CNS disorders may include Alzheimer's disease, Parkinson's disease, stroke or neuropathic pain

Sequence 1534 BP; 407 A; 362 C; 365 G; 400 T; 0 U; 0 Other;

Query Match 16.1%; Score 66; DB 9; Length 1534;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 AGGTCTGGAGTCTCCTACAGAGGATACCTTGGCCGGAGTCTCCAGTACTTAATACTACA 381  
|||||  
894 AGGTCTGGAGTCTCCTACAGAGGATACCTTGGCCGGAGTCTCCAGTACTTAATACTACA 953  
|||||

382 ATCCAG 387  
|||||

954 ATCCAG 959  
|||||

# RESULT 15

ACCT79967

ID ACC79967 standard; cDNA; 1534 BP.

ACCT79967;

09-SEP-2003 (first entry)

Human serine/threonine protein kinase encoding cDNA SEQ ID NO:1.

Human; serine/threonine protein kinase; kinase; enzyme; cytostatic; antidiabetic; neuroprotective; nootropic; antiparkinsonian; analgesic; cerebrotective; antiinflammatory; gastrointestinal; hepatotropic; gynaecological; uropathic; dermatological; gene therapy; cancer; diabetes; central nervous system disorder; CNS disorder; liver disease; respiratory disorder; chronic obstructive pulmonary disease; stroke; cardiovascular disorder; dermatological disorder; urological disorder; gastrointestinal disease; haematological disorder; Alzheimer's disease; musculoskeletal disorder; reproductive disorder; Parkinson's disease; neuropathic pain; gene; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 104..1258

/\*tag= a

/product= "serine/threonine protein kinase"

WO2003046167-A1.

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XX 05-JUN-2003.
PD
XX
XX
PF 26-NOV-2002; 2002WO-EP013268.
XX
XX
PR 27-NOV-2001; 2001US-0333131P.
XX
XX
PA (FARB ) BAYER AG.
XX
XX
PI Koehler RH;
XX
XX
DR WPI; 2003-505196/47.
DR P-PSDB; ABR57357.
XX
XX
PT New polynucleotide encoding a serine/threonine protein kinase
PT polypeptide, useful for diagnosing, preventing or treating diseases
PT associated with serine/threonine protein kinase dysfunction, e.g. cancer
PT or diabetes.
XX
PS Claim 1; Page 171-173; 196pp; English.
XX
CC The present sequence encodes a human serine/threonine protein kinase (I).
CC (I) has cytosolic, antidiabetic, neuroprotective, antiparkinsonian,
CC nootropic, cerebrotective, analgesic, antiinflammatory, hepatotropic,
CC gastrointestinal, gynaecological, uropathic and dermatological
CC activities, and can be used in gene therapy. Serine/threonine protein
CC kinase polynucleotide and polypeptide sequences can be used in
CC diagnosing, preventing, ameliorating or treating diseases associated with
CC serine/threonine protein kinase dysfunction. They may also be used to
CC identify test compounds that may act, for example, as activators or
CC inhibitors at the enzyme's active site. The human serine/threonine
CC protein kinase and its fragments are also useful in raising specific
CC antibodies that can block the enzyme and effectively reduce its activity.
CC Human serine/threonine protein kinase sequences can be used in the
CC preparation of a medicament for modulating the activity of a serine/
CC threonine protein kinase in a disease, e.g. cancer, diabetes, a central
CC nervous system (CNS) disorder, a respiratory disorder (including chronic
CC obstructive pulmonary disease), a cardiovascular disorder, a
CC dermatological disorder, a gastrointestinal or liver disease, a
CC haematological disorder, a musculoskeletal disorder, a reproductive
CC disorder, or a urological disorder. CNS disorders may include Alzheimer's
CC disease, Parkinson's disease, stroke or neuropathic pain
XX
SQ Sequence 1534 BP; 407 A; 362 C; 365 G; 400 T; 0 U; 0 Other;
Query Match 16.1%; Score 66; DB 9; Length 1534;
Best Local Similarity 100.0%; Pred. No. 1.le-10;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 322 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAGCTACCTACTACA 381
Db 894 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAGCTACCTACTACA 953
QY 382 ATCCAG 387
Db 954 ATCCAG 959

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Search completed: January 13, 2005, 02:13:23  
 Job time : 408 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2005, 01:58:49 ; Search time 2946 Seconds  
(without alignments)  
5071.382 Million cell updates/sec

Title: US-10-786-065-3\_COPY\_50000\_50409  
Perfect score: 410  
Sequence: 1 aatcatgataatcatgag.....attatgattcagcttctga 410

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsa1:\*

9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75.8	18.5	804	9	CR251670 Reverse s
2	66	16.1	481	1	AA436054 zu01c12.r
3	66	16.1	499	5	BX283916 BX283916
4	66	16.1	660	4	BX326162 602425156
5	63.4	15.5	805	9	CE137859 tigr-gsa-
6	62	15.1	602	6	CD636748 56014973J
7	60.4	14.7	598	6	CD636752 56015001J
8	60.4	14.7	602	6	CD636753 56015009H
9	58.8	14.3	600	6	CD636739 56014901H
10	58.8	14.3	602	6	CD636757 56015025H
11	58	14.1	444	2	BB640105 BB640105
12	58	14.1	502	2	BB249604 BB249604
13	52.4	12.8	586	6	CD636749 56014981H
14	52.4	12.8	601	6	CD636760 56015089J
15	51	12.4	594	9	CE640507 tigr-gsa-
16	48.4	11.8	600	6	CD636754 56015009J
17	48	11.7	600	6	CD636741 56014909H
18	46.4	11.3	314	6	CD636743 56014917H
19	46	11.2	602	6	CD636759 56015089H
20	45.8	11.2	601	6	CD636746 56014925J
21	45	11.0	599	6	CD636747 56014973H
22	44.4	10.8	602	6	CD636751 56015001H
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24	43	10.5	1494	9	AG332059 Mus muscu

C 25	42.8	10.4	596	6	CD636758
C 26	42.8	10.4	603	6	CD636742
C 27	42.6	10.4	756	9	CNS06PD3
C 28	42.6	10.4	997	9	CNS005TE
C 29	42.2	10.3	868	9	AG499155
C 30	42.2	10.3	1042	9	AG385616
C 31	42.2	10.3	1065	9	AG289256
C 32	42	10.2	1358	9	AG320427
C 33	41.4	10.1	1023	9	CL093094
C 34	41.2	10.0	812	8	B21426
C 35	41	10.0	628	5	B0592805
C 36	40.6	9.9	774	8	B19116
C 37	40.2	9.8	890	9	CNS02AC6
C 38	40	9.8	1018	5	BQ899340
C 39	39.8	9.7	401	8	AQ784003
C 40	39.6	9.7	792	4	BG565997
C 41	39.4	9.6	758	9	AG276386
C 42	39.4	9.6	1154	9	CL082790
C 43	39.2	9.6	625	8	AZ464164
C 44	39.2	9.6	730	2	BF525539
C 45	39.2	9.6	913	9	CL465943

## ALIGNMENTS

RESULT 1	CR251670	804 bp	DNA	linear	GSS 06-JUL-2004
LOCUS	Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN33n19, genomic survey sequence.				
DEFINITION	CR251670.1				
ACCESSION	CR251670.1				
VERSION	GSS; genome survey sequence; MICEP.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 804)				
AUTHORS	Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J., and Bradley,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER				
FEATURES	Location/Qualifiers				
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	/clone_lib="MHPN"				

## ORIGIN

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Best Local Similarity	83.5%;	Pred. No. 4.7e-11;		
Matches	86;	Conservative	0;	Mismatches 17;
				Indels 0;
				Gaps 0;
Qy	293	CCCTCTCTTTCTTTGTTGGCTTTATAGTCTGGAGTCCCTACAGGATACCTG	352	
Db	412	CTTACCTTTCTTTCTCTGCTCTGTAGGTTCTGGAGTCCCTACAGGATACCTG	471	
Qy	353	GCCGGAGTCTCCCAAGCTACCTAACTACCAATCCAGGTAATATT	395	
Db	472	GCTTGGAGTCTCCCAACTGCTTAATCTACATCCAGGTACGTT	514	

RESULT 2	AA436054	481 bp	mRNA	linear	EST 09-NOV-1997
LOCUS	zu01c12.r1 Soares testis NHT Homo sapiens cdna clone IMAGE:730582				
DEFINITION	5' similar to gb:X66363 SERINE/THREONINE-PROTEIN KINASE PCTAIRB-1 (HUMAN); mRNA sequence.				

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AA436054 AA436054.1 EST. Homo sapiens Homo sapiens (human)	GI:2140968	REFERENCE AUTHORS TITLE JOURNAL COMMENT	1 (bases 1 to 499) Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B. Human Unigeneset - RZPD3 Unpublished (2003) Contact: Ina Rofls RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGp9580141276 RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/cgi- bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rofls RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: pCMV-M3u, Primer sequence: CGTTGTAAACGACGCCAGT.
FEATURES source	1..499 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGp9580141276 ; IMAGE:4563301" /tissue_type="renal cell adenocarcinoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC_14" /notes="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		ORIGIN Query Match 16.1%; Score 66; DB 5; Length 499; Best Local Similarity 100.0%; Pred. No. 3.1e-08; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 322 AGGTCTGGAGTCCCTACAGAGATCTTGGCGGGAGTCTCCAGCTACCTACTACA 381 Db 113 AGGTCTGGAGTCCCTACAGAGATCTTGGCGGGAGTCTCCAGCTACCTACTACA 172 QY 382 ATCCAG 387 Db 173 ATCCAG 178	
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AA436054 AA436054.1 EST. Homo sapiens Homo sapiens (human)	GI:2140968	REFERENCE AUTHORS TITLE JOURNAL COMMENT	1 (bases 1 to 481) Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 702 Std Error: 0.00 Seq primer: -28mi3 rev2 ET from Amersham High quality sequence stop: 442. Location/Qualifiers 1..481 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:5927210" /db_xref="taxon:9606" /clone="IMAGE:730582" /sex="male" /lab_host="DH10B" /clone_lib="Soares testis NHT" /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."
FEATURES source	1..481 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:5927210" /db_xref="taxon:9606" /clone="IMAGE:730582" /sex="male" /lab_host="DH10B" /clone_lib="Soares testis NHT" /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."		ORIGIN Query Match 16.1%; Score 66; DB 1; Length 481; Best Local Similarity 100.0%; Pred. No. 3.1e-08; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 322 AGGTCTGGAGTCCCTACAGAGATCTTGGCGGGAGTCTCCAGCTACCTACTACA 381 Db 225 AGGTCTGGAGTCCCTACAGAGATCTTGGCGGGAGTCTCCAGCTACCTACTACA 284 QY 382 ATCCAG 387 Db 285 ATCCAG 290	
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCMI276 row: O column: 14  
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 Location/Qualifiers

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 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
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#### ORIGIN

Query Match 16.1%; Score 66; DB 4; Length 660;  
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 DB 171 ATCCAG 176

#### RESULT 5

CE137859 805 bp DNA linear GSS 25-SEP-2003  
 LOCUS tigr-gss-dog-17000371210778 Dog Library Canis familiaris genomic,  
 DEFINITION genomic survey sequence.  
 CE137859  
 VERSION CE137859.1 GI:35244514  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)

#### ORGANISM

Canis familiaris (dog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 805)  
 AUTHORS Kirkness E.F., Bafna V., Halpern A.L., Levy S., Remington K.,  
 Ruesch B.B., Delcher A.L., Pop M., Wang W., Fraser C.M. and  
 Venter J.C.

TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627

COMMENT Contact: Kirkness EF

The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

#### FEATURES

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 peripheral blood"

#### ORIGIN

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 DB 642 CACAGGATTTTAAGAATACATAACAGTTTGGCCCATGAACCTACAAATATGGGTGACACT 701  
 QY 162 CAAAGTTTCTTCTCGTATACATCAGCTGTGTGTCATGCAATGGGACATACCATCTGACGCT 221  
 DB 702 AAGATTTTCTTCTCGTGTGCGTCACTGGCAAAAGCGTATGATATAAAATGA----ATTAT 757  
 QY 222 TCCCTGTCTTCCCGATTTGTCCTGCATGCTCTCC 256  
 DB 758 TCCCTATTCTCCCTGATCTGTTCTTCATGCTCTCC 792

#### RESULT 6

CD636748/c  
 LOCUS CD636748 602 bp mRNA linear EST 12-JAN-2004  
 DEFINITION S6014973J1 FLP Homo sapiens cDNA, mRNA sequence.  
 ACCESSION CD636748  
 VERSION CD636748.1 GI:40285015  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

#### ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 602)  
 AUTHORS Fu G.K., Wang J.T., Yang J., Au-Young J. and Stuve L.L.  
 TITLE Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 JOURNAL Genomics 84 (1), 205-210 (2004)  
 COMMENT Contact: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com.

#### FEATURES

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 LOCUS CD636752 598 bp mRNA linear EST 12-JAN-2004  
 DEFINITION S6015001J1 FLP Homo sapiens cDNA, mRNA sequence.  
 ACCESSION CD636752  
 VERSION CD636752.1 GI:40285019  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

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Thu Jan 13 09:56:05 2005

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

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QY 322 AGGTGCTGGAGTCCCTACAGGATACCTTGGCGGGAGTCTCCAAAGCTACCTAACTACA 381
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QY 382 AT 383
Db 2 AT 1

RESULT 8
CD636753 602 bp mRNA linear EST 12-JAN-2004
LOCUS 56015009H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD636753
ACCESSION CD636753.1 GI:40285020
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

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QY 382 AT 383
Db 600 AT 601

RESULT 9
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LOCUS 56014901H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD636739
ACCESSION CD636739.1 GI:40285006
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

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Best Local Similarity 96.8%; Pred. No. 4.4e-06;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 322 AGGTGCTGGAGTCCCTACAGGATACCTTGGCGGGAGTCTCCAAAGCTACCTAACTACA 381
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QY 382 AT 383
Db 598 AT 599

RESULT 10
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LOCUS 56015025H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD636757
ACCESSION CD636757.1 GI:40285024
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
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Best Local Similarity 96.8%; Pred. No. 4.4e-06;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 322 AGGTCCTGGAGTCCCTACAGAGGATACCTTGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
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Qy 382 AT 383
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DEFINITION      BB640105 RIKEN full-length enriched, 7 days neonate cerebellum Mus
ACCESSION      BB640105
VERSION      BB640105.1 GI:15401501
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 444)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci,P., Shibata,K., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsunaga,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,
Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Funct. Genomics 2 pre, 172-186 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES
source
Location/Qualifiers
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGGAGAGAGATCTCGAGTTAAATTAATATCCCTCCCTCCCTCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
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ACCESSION      BB249604
VERSION      BB249604.2 GI:15410630
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 502)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 6, 2000 this sequence version replaced gi:8942350.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

```

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 waki, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Kira, A.,  
 Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.  
 and Hayashizaki, Y. sequence analysis (RISA) system--384-format  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multichannel sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,  
 Sugahara, Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Yamanaka, K., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A.,  
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K.,  
 Arakawa, T., Ishii, Y. and Hayashizaki, Y.  
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.  
 Funct. Genomics 2 pre, L72-L86 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp/) for  
 further details.  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
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 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGGAGGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 20.0 and subtraction to Rot = 459.0. Second  
 strand cDNA was prepared with the primer adapter of  
 sequence [5' GAGAGGAGGATTCGAGTAAATTAATTAATTCCTCCCTCC  
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 modified pBluescript KS(+) after bulk excision from Lambda  
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 1 (bases 1 to 586)  
 Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)  
 CONTACT: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com.  
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 REFERENCE  
 1 (bases 1 to 601)  
 Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)  
 CONTACT: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
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VERSION CE640507.1 GI:36958177  
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ORGANISM Canis familiaris  
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 594)  
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,M., Frazer,C.M. and  
Venter,J.C.  
TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.  
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peripheral blood"

FEATURES  
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QY 66 TCTGCCTCAGACAA 80  
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Job time : 2949 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2005, 02:05:04 ; Search time 87 Seconds  
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Total number of hits satisfying chosen parameters: 1649014

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5: /cgn2\_6/ptodata/1/ina/pCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	410	100.0	53332	4	US-10-224-562-3
3	87.4	21.3	2203	4	US-09-801-861-1
4	87.4	21.3	2203	4	US-10-224-562-1
5	66	16.1	481	3	US-09-387-212-14
6	66	16.1	481	4	US-09-948-802-14
7	66	16.1	1308	4	US-09-801-861-4
8	66	16.1	1308	4	US-10-224-562-4
9	48.2	11.8	7218	1	US-08-232-463-14
10	34.6	8.4	6405	3	US-09-281-481A-18
11	34.2	8.3	1087	3	US-08-991-789A-4
12	34.2	8.3	1087	3	US-09-062-451-4
13	34.2	8.3	1087	4	US-09-598-326-4
14	34.2	8.3	1087	4	US-09-283-198-4
15	34.2	8.3	1087	4	US-09-429-755-4
16	33.8	8.2	257	4	US-09-513-999C-34168
17	33.8	8.2	3271	3	US-08-545-196B-22
18	33.2	8.1	5152	4	US-10-204-708-48
19	33	8.0	308	4	US-09-513-999C-16871
20	32.8	8.0	31728	3	US-09-453-702B-64
21	32.6	8.0	399	4	US-09-621-976-8976
22	32.2	7.9	1044	4	US-08-956-171E-648
23	32.2	7.9	1044	4	US-08-781-986A-648
24	32	7.8	155	4	US-09-513-999C-25805
25	32	7.8	75395	4	US-09-984-890-3
26	32	7.8	75395	4	US-10-274-194-3
27	31.4	7.7	1884	4	US-09-248-796A-6511

c 28	31.4	7.7	786431	4	US-09-751-389-3	Sequence 3, Appli
c 29	31.2	7.6	273	4	US-09-313-294A-897	Sequence 897, App
c 30	31.2	7.6	292	4	US-09-313-294A-4357	Sequence 4357, Ap
c 31	31.2	7.6	451	4	US-09-513-999C-32372	Sequence 32372, A
c 32	31.2	7.6	1161	4	US-09-023-655-1373	Sequence 1373, Ap
c 33	31.2	7.6	1825	4	US-09-620-312D-313	Sequence 313, App
c 34	31.2	7.6	99500	3	US-09-798-096-10	Sequence 10, Appl
c 35	30.8	7.5	834	4	US-09-621-976-2574	Sequence 2574, Ap
c 36	30.8	7.5	53526	3	US-08-658-136-2	Sequence 2, Appli
c 37	30.8	7.5	53577	3	US-08-658-136-1	Sequence 1, Appli
c 38	30.6	7.5	248	3	US-09-007-005-32	Sequence 32, Appl
c 39	30.6	7.5	248	3	US-09-244-796-32	Sequence 32, Appl
c 40	30.6	7.5	277	3	US-09-007-005-3	Sequence 3, Appli
c 41	30.6	7.5	277	3	US-09-244-796-3	Sequence 3, Appli
c 42	30.6	7.5	338	2	US-08-454-557C-97	Sequence 97, Appl
c 43	30.6	7.5	338	2	US-08-340-426D-97	Sequence 97, Appl
c 44	30.6	7.5	338	2	US-08-450-673C-97	Sequence 97, Appl
c 45	30.6	7.5	338	5	PCT-US95-17111A-97	Sequence 97, Appl

ALIGNMENTS

RESULT 1

US-09-801-861-3  
; Sequence 3, Application US/09801861  
; Patent No. 6492154  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001098  
; CURRENT APPLICATION NUMBER: US/09/801,861  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 53332  
; TYPE: DNA  
; ORGANISM: Human  
US-09-801-861-3

Query Match	100.0%	Score 410;	DB 4;	Length 53332;
Best Local Similarity	100.0%	Pred. No. 8.2e-128;		
Matches 410;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AATCATGATTAATCATGCAAGTAAATGTTCACTGATGAGAACATGACTTTTGACGAGGCTG	60	
Db	50000	AATCATGATTAATCATGCAAGTAAATGTTCACTGATGAGAACATGACTTTTGACGAGGCTG	50059	
Qy	61	TATGATCTGCTCAGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	120	
Db	50060	TATGATCTGCTCAGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	50119	
Qy	121	ATTACAGTTTTCGCCAAGAACCAACAGTTTGGAAACACTCAAGTTTCTTCGTATA	180	
Db	50120	ATTACAGTTTTCGCCAAGAACCAACAGTTTGGAAACACTCAAGTTTCTTCGTATA	50179	
Qy	181	CATCAGCTGGTGTATGCAATGGGACATACCATCTGAGCTTCCCTGTCTTCCCTGATT	240	
Db	50180	CATCAGCTGGTGTATGCAATGGGACATACCATCTGAGCTTCCCTGTCTTCCCTGATT	50239	
Qy	241	TGTCCTCATGCTCCCAATACCTCTTTTCCCAACCACTCATCTCCCACTCCCTTCTTCTT	300	
Db	50240	TGTCCTCATGCTCCCAATACCTCTTTTCCCAACCACTCATCTCCCACTCCCTTCTTCTT	50299	
Qy	301	TTTCTTTTGGCTTTTATATAGTGTGGAGTCCCTACAGAGATACCTTTGGCGGGAG	360	
Db	50300	TTTCTTTTGGCTTTTATATAGTGTGGAGTCCCTACAGAGATACCTTTGGCGGGAG	50359	
Qy	361	TCTCAAGCTACCTAACTACCAATCCAGTAATATGATCTGAGCTTCTGA	410	

Db 50360 TCTCCAAGCTACCTAACTACATCCAGGTAATATTGATCTGAGCTTCTGA 50409

RESULT 2  
US-10-224-562-3  
; Sequence 1, Application US/10224562  
; Patent No. 6730506  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001098DIV  
; CURRENT APPLICATION NUMBER: US/10/224,562  
; CURRENT FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 53332  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-224-562-3

Query Match 100.0%; Score 410; DB 4; Length 53332;  
Best Local Similarity 100.0%; Pred. No. 8.2e-128;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGCATGATATCATGCGAGTAATCTTCAGTGATGAGAAATGCTTGGAGCAAGGCTG 60  
Db 50000 AATGCATGATATCATGCGAGTAATCTTCAGTGATGAGAAATGCTTGGAGCAAGGCTG 50059

QY 61 TATGATCTGCTCAGAACAAAGTCACTAGTAAGATGCAAGCCCGGACCATAGAAATGT 120  
Db 50060 TATGATCTGCTCAGAACAAAGTCACTAGTAAGATGCAAGCCCGGACCATAGAAATGT 50119

QY 121 ATTACAGTTTGGCCAGAAACACAAAGTTTGGAACTCAAGTTCTTCTCGTATA 180  
Db 50120 ATTACAGTTTGGCCAGAAACACAAAGTTTGGAACTCAAGTTCTTCTCGTATA 50179

QY 181 CATCAGCTGGTGTATCATGCAATGGGACATACCATCTGACCGTTCCTGTTTCCCTGATT 240  
Db 50180 CATCAGCTGGTGTATCATGCAATGGGACATACCATCTGACCGTTCCTGTTTCCCTGATT 50239

QY 241 TGTCTGCAATGCTTCCAAATACCTTTTCCAAACCACTCATCTCCCACTCACTTCTT 300  
Db 50240 TGTCTGCAATGCTTCCAAATACCTTTTCCAAACCACTCATCTCCCACTCACTTCTT 50299

QY 301 TTTCTTTTGGCTTTATATAGTGTCTGGAGTCCCTACAGAGGATCTTGGCCGGAG 360  
Db 50300 TTTCTTTTGGCTTTATATAGTGTCTGGAGTCCCTACAGAGGATCTTGGCCGGAG 50359

QY 361 TCTCCAAGCTACCTAACTACATCCAGGTAATATTGATCTGAGCTTCTGA 410  
Db 50360 TCTCCAAGCTACCTAACTACATCCAGGTAATATTGATCTGAGCTTCTGA 50409

RESULT 3  
US-09-801-861-1  
; Sequence 1, Application US/09801861  
; Patent No. 6492154  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001098  
; CURRENT APPLICATION NUMBER: US/09/801,861  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2203  
; TYPE: DNA

; ORGANISM: Human  
US-09-801-861-1

Query Match 21.3%; Score 87.4; DB 4; Length 2203;  
Best Local Similarity 98.9%; Pred. No. 2.5e-19;  
Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAGCTACCTAACTACA 381  
Db 1061 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAGCTACCTAACTACA 1120

QY 382 ATCCAGGTAATATTGATCTGAGCTTCTGA 410  
Db 1121 ATCCAGGTAATATTGATCTGAGCTTCTGA 1149

RESULT 4  
US-10-224-562-1  
; Sequence 1, Application US/10224562  
; Patent No. 6730506  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001098DIV  
; CURRENT APPLICATION NUMBER: US/10/224,562  
; CURRENT FILING DATE: 2002-08-21  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2203  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-224-562-1

Query Match 21.3%; Score 87.4; DB 4; Length 2203;  
Best Local Similarity 98.9%; Pred. No. 2.5e-19;  
Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAGCTACCTAACTACA 381  
Db 1061 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAGCTACCTAACTACA 1120

QY 382 ATCCAGGTAATATTGATCTGAGCTTCTGA 410  
Db 1121 ATCCAGGTAATATTGATCTGAGCTTCTGA 1149

RESULT 5  
US-09-387-212-14  
; Sequence 14, Application US/09387212A  
; Patent No. 6309849  
; GENERAL INFORMATION:  
; APPLICANT: ROBINSON, KEITH E.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND  
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR  
; FILE REFERENCE: MNI-090  
; CURRENT APPLICATION NUMBER: US/09/387,212A  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 481  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-387-212-14

Query Match 16.1%; Score 66; DB 3; Length 481;  
Best Local Similarity 100.0%; Pred. No. 2e-12;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGAGTCTCCAAGCTACCTAACTACA 381



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Db 225 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 284
Qy 382 ATCCAG 387
Db 285 ATCCAG 290

RESULT 6
US-09-948-802-14
; Sequence 14, Application US/09948802
; Patent No. 6465232
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-948-802-14

Query Match 16.1%; Score 66; DB 4; Length 481;
Best Local Similarity 100.0%; Pred. No. 2e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 66; Conservative 0;

Qy 322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 381
Db 225 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 284
Qy 382 ATCCAG 387
Db 285 ATCCAG 290

RESULT 7
US-09-801-861-4
; Sequence 4, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Release 1.0, Version #1.25
; SEQ ID NO 4
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Human
US-09-801-861-4

Query Match 16.1%; Score 66; DB 4; Length 1308;
Best Local Similarity 100.0%; Pred. No. 3.3e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 66; Conservative 0;

Qy 322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 381
Db 944 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 1003
Qy 382 ATCCAG 387
Db 1004 ATCCAG 1009

RESULT 8
US-10-224-562-4
; Sequence 4, Application US/10224562
; Patent No. 6730506
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Human
US-10-224-562-4

Query Match 16.1%; Score 66; DB 4; Length 1308;
Best Local Similarity 100.0%; Pred. No. 3.3e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 66; Conservative 0;

Qy 322 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 381
Db 944 AGGTCTGGAGTCCCTACAGAGGATACCTTGGCCGGAGTCTCCAAAGCTACCTAACTACA 1003
Qy 382 ATCCAG 387
Db 1004 ATCCAG 1009

RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOMLOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
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; LENGTH: 6405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-09-281-481A-18

Query Match      8.4%; Score 34.6; DB 3; Length 6405;
Best Local Similarity 51.6%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 74;

186  GCTGGTGTGCATGCGAGACATACCATCTGACGCTTCCCTGTGTTCCCTCGATTGTGCC 245
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
4850  GCATGTCTTAGCGARAGCCCCCTGTGCAAGTTCCTTCTCTGTGCGTCGACGAGCTTCTT 4791

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246  TGCATGTCTCCAATACCTCTTTTCCAAACCACTCATCTCCCACTTCACCTTCTTTTTTCT 305
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
4790  TTGTTTGAATAAATTCAACTGAGAACCCACCACCACTACTGCCGCCCTGCACGAGTTTCTTCT 4731
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

306  TTGTTTGGCTTTATATAGTGCTGGGAGTCCCT 338
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
4730  TTTTTTCTCTCTCAATTTGTGTATGATTTCCT 4698
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RESULT 11  
US-08-991-789A-4  
; Sequence 4, Application US/08991789A  
; Patent No. 6,225,054  
; GENERAL INFORMATION:  
; APPLICANT: Fridakis, Tony N.  
; Smith, John M.  
; Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; DIAGNOSIS OF BREAST CANCER

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Db 189 ACCTCAGGCTCCACCATACCCAGAGTGTCTGGTTTGTAAATTACTGCCAGGTT 248  
Qy 334 TCCCTACAGAGATACCTTGGCCGGGAGTCTCCAGCTACCTTAACCTACCAATCCAGGTAATA 393  
Db 249 TCAGCTCAGAGATATCCCTGGGAAGAAATATCCAGATTCCTCGTAGTGTTCAGGTTAAA 308  
Qy 394 TTGATCTGAGCTTCT 408  
Db 309 ATCTATAGGCTTCT 323

RESULT 12  
US-09-062-451-4  
; Sequence 4, Application US/09062451  
; Patent No. 6344550  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Smith, John M.  
; APPLICANT: Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 297  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/062,451  
; FILING DATE: 04-APR-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.419C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1087 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-062-451-4

Query Match 8.3%; Score 34.2; DB 3; Length 1087;  
Best Local Similarity 53.3%; Pred. No. 0.17; Mismatches 63; Indels 0; Gaps 0;  
Matches 72; Conservative 0

Qy 274 ACCTCATCTCCACCTCACCTTTCTTTTCTTTGGCTTTATATAGGTGCTGGGAG 333  
Db 189 ACCTCAGGCTCCACCATACCCAGAGTGTCTGGTTTGTAAATTACTGCCAGGTT 248  
Qy 334 TCCCTACAGAGATACCTTGGCCGGGAGTCTCCAGCTACCTTAACCTACCAATCCAGGTAATA 393  
Db 249 TCAGCTCAGAGATATCCCTGGGAAGAAATATCCAGATTCCTCGTAGTGTTCAGGTTAAA 308  
Qy 394 TTGATCTGAGCTTCT 408  
Db 309 ATCTATAGGCTTCT 323

RESULT 13  
US-09-598-326-4  
; Sequence 4, Application US/09598326

; Patent No. 6423496  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Smith, John M.  
; APPLICANT: Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 247  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed Intellectual Property Law Group PLLC  
; STREET: 701 Fifth Avenue, Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/598,326  
; FILING DATE: 20-Jun-2000  
; CLASSIFICATION: <unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E.R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 210121.419D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1087 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-598-326-4

Query Match 8.3%; Score 34.2; DB 4; Length 1087;  
Best Local Similarity 53.3%; Pred. No. 0.17; Mismatches 63; Indels 0; Gaps 0;  
Matches 72; Conservative 0

Qy 274 ACCTCATCTCCACCTCACCTTTCTTTTCTTTGGCTTTATATAGGTGCTGGGAG 333  
Db 189 ACCTCAGGCTCCACCATACCCAGAGTGTCTGGTTTGTAAATTACTGCCAGGTT 248  
Qy 334 TCCCTACAGAGATACCTTGGCCGGGAGTCTCCAGCTACCTTAACCTACCAATCCAGGTAATA 393  
Db 249 TCAGCTCAGAGATATCCCTGGGAAGAAATATCCAGATTCCTCGTAGTGTTCAGGTTAAA 308  
Qy 394 TTGATCTGAGCTTCT 408  
Db 309 ATCTATAGGCTTCT 323

RESULT 14  
US-09-289-198-4  
; Sequence 4, Application US/09289198  
; Patent No. 6586570  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Smith, John M.  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Misher, Lynda  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.419C5  
; CURRENT APPLICATION NUMBER: US/09/289,198  
; CURRENT FILING DATE: 1999-04-09  
; EARLIER APPLICATION NUMBER: US 09/062,451  
; EARLIER FILING DATE: 1998-04-17

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EARLIER APPLICATION NUMBER: US 08/991,789  
EARLIER FILING DATE: 1997-12-11  
EARLIER APPLICATION NUMBER: US 08/838,762  
EARLIER FILING DATE: 1997-04-09  
EARLIER APPLICATION NUMBER: PCT/US97/00485  
EARLIER FILING DATE: 1997-01-10  
EARLIER APPLICATION NUMBER: US 08/700,014  
EARLIER FILING DATE: 1996-08-20  
EARLIER APPLICATION NUMBER: US 08/585,392  
EARLIER FILING DATE: 1996-01-01  
NUMBER OF SEQ ID NOS: 312  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 1087  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1087)  
OTHER INFORMATION: n = A,T,C or G

US-09-289-198-4

Query Match 8.3%; Score 34.2; DB 4; Length 1087;  
Best Local Similarity 53.3%; Pred. No. 0.17; Indels 0; Gaps 0;  
Matches 72; Conservative 0; Mismatches 63;  
QY 274 ACCTCATCTCCACCTCACCCTTTCTTTTCTTTGGCTTATATAGGTGCTGGAG 333  
DB 189 ACCTCAGGCTCCAAACCATACCCCAAGAGTTGTTGGTTTAAATTACTGCCAGTT 248  
QY 334 TCCCTACAGAGGATCTTGGCCGGAGTCTCCAAAGCTACCTAACTACCAATCCAGTAATA 393  
DB 249 TCAGCTGCGAGATATCCCTCGAAGGAATATTCCAGATTCCCTGAGTAGTTCCAGTTAAA 308  
QY 394 TTGATCTGAGCTTCT 408  
DB 309 ATCTATAGGCTTCT 323

RESULT 15  
US-09-429-755-4  
Sequence 4, Application US/09429755A  
Patent No. 6656480  
GENERAL INFORMATION:  
APPLICANT: Frudakis, Tony N.  
APPLICANT: Smith, John M.  
APPLICANT: Reed, Steven G.  
APPLICANT: Mishner, Lynda  
APPLICANT: Retter, Marc W.  
APPLICANT: Dillon, Davin C.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.419C6  
CURRENT APPLICATION NUMBER: US/09/429,755A  
CURRENT FILING DATE: 1999-10-28  
NUMBER OF SEQ ID NOS: 315  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 1087  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1087)  
OTHER INFORMATION: n = A,T,C or G

US-09-429-755-4  
Query Match 8.3%; Score 34.2; DB 4; Length 1087;  
Best Local Similarity 53.3%; Pred. No. 0.17; Indels 0; Gaps 0;  
Matches 72; Conservative 0; Mismatches 63;  
QY 274 ACCTCATCTCCACCTCACCCTTTCTTTTCTTTGGCTTATATAGGTGCTGGAG 333

Db 189 ACCTCAGGCTCCAAACCATACCCCAAGAGTTGTTGGTTTAAATTACTGCCAGTT 248  
QY 334 TCCCTACAGAGGATCTTGGCCGGAGTCTCCAAAGCTACCTAACTACCAATCCAGTAATA 393  
DB 249 TCAGCTGCGAGATATCCCTCGAAGGAATATTCCAGATTCCCTGAGTAGTTCCAGTTAAA 308  
QY 394 TTGATCTGAGCTTCT 408  
DB 309 ATCTATAGGCTTCT 323

Search completed: January 13, 2005, 03:36:42  
Job time : 89 secs

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	410	100.0	53332	9	US-09-801-861-3	Sequence 3, Appli
2	410	100.0	53332	14	US-10-224-562-3	Sequence 3, Appli
3	87.4	21.3	2203	9	US-09-801-861-1	Sequence 1, Appli
4	87.4	21.3	2203	14	US-10-224-562-1	Sequence 1, Appli
5	66	16.1	481	9	US-09-948-802-14	Sequence 14, Appli
6	66	16.1	481	15	US-10-121-925-14	Sequence 14, Appli
7	66	16.1	1308	9	US-09-801-861-4	Sequence 4, Appli
8	66	16.1	1308	14	US-10-224-562-4	Sequence 4, Appli
9	66	16.1	1376	16	US-10-466-759-15	Sequence 15, Appli
10	66	16.1	2250	18	US-10-618-941-20	Sequence 20, Appli
11	66	16.1	3210	16	US-10-425-114-26244	Sequence 26244, A
12	38.2	9.3	113515	15	US-10-311-455-2148	Sequence 2148, Ap

## ALIGNMENTS

Query Match

db 50120 ATTACAGTATTGCCCCAAGAAACCAAAACGTTGGAAACACTCAAGTTTCTTTCTCGTATA 50179

Thu Jan 13 09:56:04 2005

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; Sequence 1, Application US/09801861
; Patent No. US20020119544A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2203
; TYPE: DNA
; ORGANISM: Human
; US-09-801-861-1

Query Match      21.3%; Score 87.4; DB 9; Length 2203;
Best Local Similarity 98.9%; Pred. No. 1.7e-18; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 1;

QY 322 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 1061 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 1120
QY 382 ATCCAGGTAATATTGATCTGAGCTTCTGA 410
DB 1121 ATCCAGGTAATATTGATCTGAGCTTCTGA 1149

RESULT 4
US-10-224-562-1
; Sequence 1, Application US/10224562
; Publication No. US2003002229A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2203
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-224-562-1

Query Match      21.3%; Score 87.4; DB 14; Length 2203;
Best Local Similarity 98.9%; Pred. No. 1.7e-18; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 1;

QY 322 AGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381
DB 1061 AGGTGCTGGAGTCCCTACAGAGGATCTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 1120
QY 382 ATCCAGGTAATATTGATCTGAGCTTCTGA 410
DB 1121 ATCCAGGTAATATTGATCTGAGCTTCTGA 1149

RESULT 5
US-09-948-802-14
; Sequence 14, Application US/09948802
; Publication No. US20020172981A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; US-09-801-861-1
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QY 181 CATGAGCTGGTGCATGCAATGGGACATACATCTGACGCTTCCCTGTTCTTCCCTGATT 240
DB 50180 CATGAGCTGGTGCATGCAATGGGACATACATCTGACGCTTCCCTGTTCTTCCCTGATT 50239
QY 241 TGTCTGATGCTCTCCAACTCTTTCCAAACACCTCATCTCTCCACCTCAGCTTTCTT 300
DB 50240 TGTCTGATGCTCTCCAACTCTTTCCAAACACCTCATCTCTCCACCTCAGCTTTCTT 50299
QY 301 TTTCTTTGTTGGCTTTATATAGTGTGGGAGTCCCTACAGAGGATCTTGGCCGGGAG 360
DB 50300 TTTCTTTGTTGGCTTTATATAGTGTGGGAGTCCCTACAGAGGATCTTGGCCGGGAG 50359
QY 361 TCTCCAAGCTACCTAACTACAACTCAGGTAATATTGATCTGAGCTTCTGA 410
DB 50360 TCTCCAAGCTACCTAACTACAACTCAGGTAATATTGATCTGAGCTTCTGA 50409

RESULT 2
US-10-224-562-3
; Sequence 3, Application US/10224562
; Publication No. US2003002229A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-224-562-3

Query Match      100.0%; Score 410; DB 14; Length 53332;
Best Local Similarity 100.0%; Pred. No. 1.2e-127; Indels 0; Gaps 0;
Matches 410; Conservative 0; Mismatches 0;

QY 1 AATGCATGTAATCATGTCAGTAATGTTCAAGTATGAGAACATGATCTTGGAGCAAGGCTG 60
DB 50000 AATGCATGTAATCATGTCAGTAATGTTCAAGTATGAGAACATGATCTTGGAGCAAGGCTG 50059
QY 61 TATGATCTGCCTCAGAACAAAGTGAGTCAAGTATGAGAACATGAGGCTG 120
DB 50060 TATGATCTGCCTCAGAACAAAGTGAGTCAAGTATGAGAACATGAGGCTG 50119
QY 121 ATTACAGTTTGGCCCAAGAACCAACCAACGTTGGAAACACTCAAGTTTCTTCGTATA 180
DB 50120 ATTACAGTTTGGCCCAAGAACCAACCAACGTTGGAAACACTCAAGTTTCTTCGTATA 50179
QY 181 CATCAGCTGGTGCATGCAATGGGACATACCATCTGACGCTTCCCTGTTCTTCCCTGATT 240
DB 50180 CATCAGCTGGTGCATGCAATGGGACATACCATCTGACGCTTCCCTGTTCTTCCCTGATT 50239
QY 241 TGTCTGCAATGCTCCAACTCTTTCCAAACACCTCATCTCTCCACCTCAGCTTTCTT 300
DB 50240 TGTCTGCAATGCTCCAACTCTTTCCAAACACCTCATCTCTCCACCTCAGCTTTCTT 50299
QY 301 TTTCTTTGTTGGCTTTATATAGTGTGGGAGTCCCTACAGAGGATCTTGGCCGGGAG 360
DB 50300 TTTCTTTGTTGGCTTTATATAGTGTGGGAGTCCCTACAGAGGATCTTGGCCGGGAG 50359
QY 361 TCTCCAAGCTACCTAACTACAACTCAGGTAATATTGATCTGAGCTTCTGA 410
DB 50360 TCTCCAAGCTACCTAACTACAACTCAGGTAATATTGATCTGAGCTTCTGA 50409

RESULT 3
US-09-801-861-1
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; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-948-802-14

Query Match          16.1%; Score 66; DB 9; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTGCTGGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCCAAGCTACCTAACTACA 381
DB 225 AGGTGCTGGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCCAAGCTACCTAACTACA 284

QY 382 ATCCAG 387
DB 285 ATCCAG 290

RESULT 6
US-10-121-925-14
; Sequence 14, Application US/10121925
; Publication No. US20030104505A1
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/10/121,925
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/948,802
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-121-925-14

Query Match          16.1%; Score 66; DB 15; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTGCTGGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCCAAGCTACCTAACTACA 381
DB 225 AGGTGCTGGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCCAAGCTACCTAACTACA 284

QY 382 ATCCAG 387
DB 285 ATCCAG 290

RESULT 7
US-09-801-861-4
; Sequence 4, Application US/09801861
; Patent No. US20020119544A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09

; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Human
US-09-801-861-4

Query Match          16.1%; Score 66; DB 9; Length 1308;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTGCTGGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCCAAGCTACCTAACTACA 381
DB 944 AGGTGCTGGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCCAAGCTACCTAACTACA 1003

QY 382 ATCCAG 387
DB 1004 ATCCAG 1009

RESULT 8
US-10-224-562-4
; Sequence 4, Application US/10224562
; Publication No. US2003002229A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Human
US-10-224-562-4

Query Match          16.1%; Score 66; DB 14; Length 1308;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGGTGCTGGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCCAAGCTACCTAACTACA 381
DB 944 AGGTGCTGGGAGTCCCTACAGAGGATACCTTGGCCGGGAGTCTCCCAAGCTACCTAACTACA 1003

QY 382 ATCCAG 387
DB 1004 ATCCAG 1009

RESULT 9
US-10-466-759-15
; Sequence 15, Application US/10466759
; Publication No. US20040081983A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: LEE, Ernestine A.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: ISON, Craig H.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: JACKSON, Jennifer L.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: TRAN, Bao
; APPLICANT: DING, Li
; APPLICANT: LU, Dying Aina M.
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Thu Jan 13 09:56:04 2005

APPLICANT: LAL, Preeti G.  
APPLICANT: WARREN, Bridget A.  
TITLE OF INVENTION: KINASES AND PHOSPHATASES  
FILE REFERENCE: PI-0344 USN  
CURRENT APPLICATION NUMBER: US/10/466,759  
CURRENT FILING DATE: 2003-07-17  
PCT/US02/01369  
PRIOR APPLICATION NUMBER: 2002-01-16  
PRIOR FILING DATE: 2002-01-16  
PRIOR APPLICATION NUMBER: US 60/263,083  
PRIOR FILING DATE: 2001-01-18  
PRIOR APPLICATION NUMBER: US 60/271,205  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: US 60/271,117  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: US 60/276,859  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: US 60/278,504  
PRIOR FILING DATE: 2001-03-23  
PRIOR APPLICATION NUMBER: US 60/278,522  
PRIOR FILING DATE: 2001-03-23  
PRIOR APPLICATION NUMBER: US 60/280,510  
PRIOR FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: US 60/280,266  
PRIOR FILING DATE: 2001-03-29  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PERL Program  
SEQ ID NO 15  
LENGTH: 1376  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: 7494145CB1  
US-10-466-759-15

Query Match 16.1%; Score 66; DB 16; Length 1376;  
Best Local Similarity 100.0%; Pred. No. 2.7e-11; Indels 0; Gaps 0;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 322 AGTGCTGGAGTCCCTACAGAGTACTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381  
DB 1088 AGTGCTGGAGTCCCTACAGAGTACTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 1147  
QY 382 ATCCAG 387  
DB 1148 ATCCAG 1153

RESULT 10  
US-10-618-941-20  
Sequence 20, Application US/10618941  
Publication No. US20040197792A1  
GENERAL INFORMATION:  
APPLICANT: WHYTE, DAVID  
APPLICANT: MANNING, GERARD  
APPLICANT: CAENEPEEL, SEAN  
TITLE OF INVENTION: NOVEL KINASES  
FILE REFERENCE: 034536-0321  
CURRENT APPLICATION NUMBER: US/10/618,941  
CURRENT FILING DATE: 2003-07-15  
PRIOR APPLICATION NUMBER: 60/395,632  
PRIOR FILING DATE: 2002-07-15  
NUMBER OF SEQ ID NOS: 143  
SOFTWARE: Patent version 3.2  
SEQ ID NO 20  
LENGTH: 2250  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-618-941-20

Query Match 16.1%; Score 66; DB 18; Length 2250;  
Best Local Similarity 100.0%; Pred. No. 3.4e-11;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGTGCTGGAGTCCCTACAGAGTACTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381  
DB 988 AGTGCTGGAGTCCCTACAGAGTACTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 1047  
QY 382 ATCCAG 387  
DB 1048 ATCCAG 1053

RESULT 11  
US-10-425-114-26244  
Sequence 26244, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 26244  
LENGTH: 3210  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB4119-079-Cl\_FLI  
US-10-425-114-26244

Query Match 16.1%; Score 66; DB 16; Length 3210;  
Best Local Similarity 100.0%; Pred. No. 4.1e-11; Indels 0; Gaps 0;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 AGTGCTGGAGTCCCTACAGAGTACTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 381  
DB 560 AGTGCTGGAGTCCCTACAGAGTACTTGGCCGGGAGTCTCCAAAGCTACCTAACTACA 619  
QY 382 ATCCAG 387  
DB 620 ATCCAG 625

RESULT 12  
US-10-311-455-2148/c  
Sequence 2148, Application US/10311455  
Publication No. US20030143606A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENBROCK, Christian  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ  
TITLE OF INVENTION: cytosine methylation  
FILE REFERENCE: 5013.1014  
CURRENT APPLICATION NUMBER: US/10/311,455  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/EP01/07537  
PRIOR FILING DATE: 2001-07-02  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 2424  
SEQ ID NO 2148  
LENGTH: 113515  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:



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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2148

Query Match          9.3%; Score 38.2; DB 15; Length 113515;
Best Local Similarity 55.7%; Pred. No. 0.67;
Matches 73; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 191 TGTGATGCAATGGGACATACCATCGAGCTTCCTGTTCTTCCTGATTTGCTGCTCAT 250
Db 61960 TTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 61901

Qy 251 GTCTCCAATACCTCTTTCAACCACTCATCTCCCACTCACTCACTTTCTTTCTTTCTTT 310
Db 61900 TCCCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 61841

Qy 311 TGGCTTTTATAT 321
Db 61840 TCTCTTTCTCT 61830

RESULT 13
US-10-021-323-798/c
; Sequence 798, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 798
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3825-013-Q1-N6-A6
US-10-021-323-798

Query Match          9.0%; Score 37; DB 17; Length 543;
Best Local Similarity 60.4%; Pred. No. 0.13;
Matches 61; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 221 TTCCTGTTCTTCCCTGATTTGCTGCTGATGTTCTCCAAATACCTCTTTCCAAACCACTCAT 280
Db 422 TTCCTCTTTTGGCCCATTTCTCTTCCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTT 363

Qy 281 CTCCCACTCACTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTATAT 321
Db 362 CCCCCTTTCTCCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTT 322

RESULT 14
US-09-796-692-3640/c
; Sequence 3640, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
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; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3640
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-3640

Query Match          8.9%; Score 36.4; DB 9; Length 285;
Best Local Similarity 58.2%; Pred. No. 0.15;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 221 TTCCTGTTCTTCCCTGATTTGCTGCTGATGTTCTCCAAATACCTCTTTCCAAACCACTCAT 280
Db 110 TTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 51

Qy 281 CTCCCACTCACTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTATATAGTGTGG 330
Db 50 CTCCTGCCCCAACATCTCTGTGCCATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGG 1

RESULT 15
US-10-040-862-3640/c
; Sequence 3640, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
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us-10-786-065-3\_copy\_50000\_50409.rnpb

Thu Jan 13 09:56:04 2005

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; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3640
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-040-862-3640

Query Match      8.9%; Score 36.4; DB 14; Length 285;
Best Local Similarity 58.2%; Pred. No. 0.15; 46; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 46;

Qy 221 TTCCCTGTTCTCCCTGATTGCTGCATGTCCTCAATACCTCTTTCCACGACCTCAT 280
Db 110 TTCCCTGTTCTCCCTGATTGCTGCATGTCCTCAATACCTCTTTCCACGACCTCAT 280
Qy 281 CTCGCCACCTCACCTTTCTTTCTTTGTTGCTTTATATAGGTGCTGG 330
Db 50 CTCGCTGCCCAACATCCTGTGCCATCCCTGTGTGTGTGTTGGTCTTGG 1

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Search completed: January 13, 2005, 07:01:54  
Job time : 4988 secs